

FIG. 1A

AGGGGGCGCGTGGATGCGGCGGAGCTGAAGCCTCGAGCAGCGGCGCTTCT  
 -120  
 GGCTGCCGG

CTGGCCCCGGCCATATGGCTTGAAGAGCCGTGCCACCCAGTGGCCCCACTGCCCA  
 -1

1 Met Asp Pro Leu Asn Leu Ser Trp Tyr Asp Asp Leu Glu Arg  
 ATG GAT CCA CCA CTG AAC CTG TCC TCG TAC GAT GAC GAT CTG GAG AGG  
 10

\* 20 \* 30  
 Gln Asn Trp Ser Arg Pro Phe Asn Gly Ser Glu Gly Lys Ala Asp  
 CAG AAC TGG AGC CGG CCC TTC AAT GGG TCA GAA GGG AAG GCA GAC  
 40 90

Arg Pro His Tyr Asn Tyr Tyr Ala Met Leu Leu Thr Leu Ile  
 AGG CCC CAC TAC AAC AAC TAC TAT GCC ATG CTG CTC ACC CTC CTC ATC

50 60  
 Phe Ile Ile Val Phe Gly Asn Val Leu Val Cys Met Ala Val Ser  
 TTT ATC ATC GTC TTT GGC AAT-GTG CTG CTG GTG TGC ATG GCT GTA TCC  
 180

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Glu | Lys | Ala | Leu | Gln | Thr | Thr | Thr | Asn | Tyr | Leu | Ile | Val | Ser |
| GCA | GAG | AAG | GCT | TTG | CAG | ACC | ACC | ACC | AAC | TAC | TTG | ATA | GTC | AGC |
| 70  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Leu | Ala | Val | Ala | Asp | Leu | Leu | Val | Ala | Thr | Leu | Val | Met | Pro | Trp |
| CTT | GCT | GTG | GCT | GAT | CTT | CTG | GTG | GCC | ACA | CTG | GTA | ATG | CCG | TGG |
| 80  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Val | Val | Tyr | Leu | Glu | Val | Val | Gly | Glu | Trp | Lys | Phe | Ser | Arg | Ile |
| GTT | GTC | TAC | CTG | GAG | GTG | GTG | GGT | GAG | TGG | AAA | TTC | AGC | AGG | ATT |
| 100 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| His | Cys | Asp | Ile | Phe | Val | Thr | Leu | Asp | Val | Met | Met | Cys | Thr | Ala |
| CAC | TGT | GAC | ATC | TTT | GTC | ACT | CTG | GAT | GTC | ATG | ATG | TGC | ACA | GCA |
| 110 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Ser | Ile | Leu | Asn | Leu | Cys | Ala | Ile | Ser | Ile | Asp | Arg | Tyr | Thr | Ala |
| AGC | ATC | CTG | AAC | CTG | TGT | GCC | ATC | AGC | ATT | GAC | AGG | TAC | ACA | GCT |
| 130 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Val | Ala | Met | Pro | Met | Leu | Tyr | Asn | Thr | Arg | Tyr | Ser | Ser | Lys | Arg |
| GTG | GCA | ATG | CCC | ATG | CTG | TAT | AAC | ACA | CGC | TAC | AGC | TCC | AAG | CGC |
| 140 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 150 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 450 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

FIG. 1B

|            |            |            |            |            |            |            |            |            |            |     |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|-----|------------|------------|------------|------------|------------|
| Arg<br>CGA | Val<br>GTT | Thr<br>ACT | Val<br>GTC | Met<br>ATG | Ile<br>ATT | Ala<br>GCC | Ile<br>ATT | Val<br>GTC | Trp<br>TGG | 160 | Val<br>GTC | Leu<br>CTG | Ser<br>TCC | Phe<br>TTC | Thr<br>ACC |
| Ile<br>ATC | Ser<br>TCC | Cys<br>TGC | Pro<br>CCA | Leu<br>CTG | Leu<br>CTC | Phe<br>TTC | Gly<br>GGA | Leu<br>CTC | Asn<br>AAC | 170 | Asn<br>AAT | Thr<br>ACA | Asp<br>GAC | Gln<br>CAG | 180        |
| Glu<br>GAG | Cys<br>TGT | Ile<br>ATC | Ile<br>ATT | Ala<br>GCC | Asn<br>AAC | Pro<br>CCT | Ala<br>GCC | Phe<br>TTT | Val<br>GTG | 190 | Val<br>GTC | Tyr<br>TAC | Ser<br>TCC | Ser<br>TCC | Ile<br>ATT |
| Val<br>GTC | Ser<br>TCA | Phe<br>TTC | Tyr<br>TAC | Val<br>GTG | Pro<br>CCC | Phe<br>TTC | Ile<br>ATC | Val<br>GTC | Thr<br>ACT | 200 | Leu<br>CTG | Leu<br>CTG | Val<br>GTC | Tyr<br>TAT | 210        |
| Lys<br>AAA | Ile<br>ATC | Tyr<br>TAC | Ile<br>ATC | Val<br>GTC | Leu<br>CTC | Arg<br>CGG | Lys<br>AAG | Arg<br>CGC | Arg<br>CGG | 220 | Lys<br>AAG | Arg<br>CGG | Val<br>GTC | Asn<br>AAC | Thr<br>ACC |
| Lys<br>AAG | Arg<br>CGC | Ser<br>AGC | Ser<br>AGT | Arg<br>CGA | Ala<br>GCT | Phe<br>TTC | Arg<br>AGA | Ala<br>GCC | Asn<br>AAC | 230 | Leu<br>CTG | Lys<br>AAG | Thr<br>ACA | Pro<br>CCA | 240        |
|            |            |            |            |            |            |            |            |            |            |     |            |            |            |            | Leu<br>CTC |
|            |            |            |            |            |            |            |            |            |            |     |            |            |            |            | 720        |

FIG. 1C

|  |             |
|--|-------------|
| Lys Asp Ala Ala Arg Arg Ala Gln Glu Leu Glu Met Glu Met Leu<br>AAG GAT GCT GCC CGC CGA GCT CAG CAG GAG CTG GAA ATG GAG ATG CTG     | 250         |
| Ser Ser Thr Ser Ser Pro Pro Glu Arg Thr Arg Tyr Ser Ser Pro Ile Pro<br>TCA AGC ACC AGC CCC CCA CAG AGG ACC CGG TAT AGC CCC ATC CCT | 260 270     |
| Pro Ser His His Gln Leu Thr Leu Pro Asp Pro Ser His His Gly<br>CCC AGT CAC CAC CAG CTC ACT CTC CCT GAT CCA TCC CAC CAC GGC         | 280 810     |
| Leu His Ser Asn Pro Pro Ser Pro Ala Lys Lys Pro Gly Lys Asn Gly<br>CTA CAT AGC AAC CCT GAC AGT CCT GCC GCC AAA CCA GAG AAG AAT GGG | 290 300     |
| His Ala Lys Ile Val Asn Pro Arg Ile Ala Lys Phe Phe Glu Ile<br>CAC GCC AAG ATT GTC AAT CCC AGG ATT GCC AAG AAC TTC TTT GAG ATC     | 310 900     |
| Gln Thr Met Pro Asn Gly Lys Thr Arg Thr Ser Leu Lys Thr Met<br>CAG ACC ATG CCC AAT GGC AAA ACC CGG ACC TCC CTT AAG ACG ATG         | 320 330 990 |

FIG. 1D

|     |     |     |     |     |     |     |     |     |     |                       |     |     |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----------------------|-----|-----|------|
| Ser | Arg | Arg | Lys | Leu | Ser | Gln | Gln | Lys | Lys | Ala                   | Thr | Gln | 340  |
| AGC | CGC | AGA | AAG | CTC | TCC | CAG | CAG | AAG | AAA | GCC                   | ACT | CAG |      |
| Met | Leu | Ala | Ile | Val | Leu | Gly | Val | Phe | Ile | Cys                   | Trp | Leu | 360  |
| ATG | CTT | GCC | ATT | GTT | CTC | GGT | GTG | TTC | ATC | TGC                   | TGG | CTG | Pro  |
|     |     |     |     |     |     |     |     |     |     |                       |     |     | 1080 |
| Phe | Phe | Ile | Thr | His | Ile | Leu | Asn | Ile | Cys | Asp                   | Cys | Asn | 370  |
| TTC | TTC | ATC | ACG | CAC | ATC | CTG | AAT | ATA | TGT | GAT                   | TGC | AAC | Ile  |
|     |     |     |     |     |     |     |     |     |     |                       |     |     | ATC  |
| Pro | Pro | Val | Leu | Tyr | Ser | Ala | Phe | Thr | Trp | Gly                   | Tyr | Val | 390  |
| CCA | CCA | GTC | CTC | TAC | AGC | GCC | TTC | ACA | TGG | CTG                   | TAT | GTC | Asn  |
|     |     |     |     |     |     |     |     |     |     |                       |     |     | AAC  |
|     |     |     |     |     |     |     |     |     |     |                       |     |     | 1170 |
| Ser | Ala | Val | Asn | Pro | Ile | Ile | Tyr | Thr | Thr | Asn                   | Ile | Glu | 400  |
| AGT | GCC | GTC | AAC | CCC | ATC | ATC | TAC | ACC | ACC | AAC                   | ATC | GAG | Phe  |
|     |     |     |     |     |     |     |     |     |     |                       |     |     | TTC  |
| Arg | Lys | Ala | Phe | Met | Lys | Ile | Leu | His | TGC | TGAGTCTGCCCCCTTGCCCTG |     |     | 1264 |
| CGC | AAG | GCC | TTC | ATG | AAG | ATC | TTG | CAC |     |                       |     |     |      |

FIG. 1E

CACAGCAGCTGCTTCCCACCTCCCTGCCTATGCAGGCCAGACCTCATCCCTGCAAGCTG  
TGGGCAGAAAGGCCAGATGAACCTTGGCCTTCTCTCGACCCCTGCAGGCCCTGCAGTGTTA  
GCTTGGCTCGATGCCCTCTCTGCCCACACACCCTCATCCTGCCAGGGTAGGGCCAGGG 1383  
AGACTGGTATCTTACCAGCTCTGGGGTTGGACCCATGGCTCAGGGCAGCTCACAGAGTGC  
CCCTCTATATCCAGACCCTGTCTCCTTGGCACCAAGATGCAGCGGCTTCCCTTGACC 1502  
TTCCTCTTGGGCACAGAACTAGCTCAGTGGTCGAGCACACCCTGATCGCTGGCTTGGCC  
TGGCCCTTGCTTGCCCTGTGCCGGATCAGGTGGTGGAGGGAGCGACACGTTCTTACTTT 1621  
ATAGGAACCACATAGGAAGCAGGGAACACGCCAAGTCCTCCAGGCACATCAGTGTGAGG 1740  
AGACACACATAAACACACAGGTAGCTCCATGGACCCAGAGAACTGAGGCTGAAAAATC  
TGTTTCCACTCCAACCTAGTGTGAGTCCCTACTTTTCATAGCCATGGGTATTACTATG 1859

FIG. 1F

TCCTACCTTGTTATAGTATCCCATGGGGTTTCTGTACCATTTGGGGAAACAACCTA  
 ATCCTCAAGGGCCCCAAGAGAACTCTGTAAGGAGAAAATAGGCTGATCTCCCTCTACTCT  
 CCAATCCACTCCACCCTTCTTGATATACCTTGGATGTATCCATTCCCTCACAGCAAATG 1978  
 CTGGCCAGTCAGGCCTTGGACCAGTGTGGAGTTGAAGCTGGATGTGGTAACTTGGGGCT  
 CTTTGGGCTGGGGGGTGTAAACATCGTCTCTCTTCCATATCTCTTCCCTTCCCAGTG 2097  
 CCTCTGCCCTTAGAAGAGGCTGTGGATGGGGTGGTGGCTGATACCATTTGGGCCTGG  
 CCCTGAATGAGGAGGGGAAGCTGCAGTTTGGAGGGTTCTGGGATCCAACTCTGTAAACAT 2216  
 CACTATACCTGTACCAAAACCTAATAAAAACCTTGACAAGAGTCAAAAA  
 AAAAAA 2317

FIG. 1G



FIG. 2

D<sub>6</sub>  
β<sub>6</sub>  
α<sub>6</sub>  
G-21  
M<sub>1</sub>  
SK

I  
MD...PL...NISWYDDDLERQNSRPFNGSEKADRPYNYAMII...IFIIVFGNVLCMAVSREKALQITITNY  
MGP...P...GNDSDFLLTNGSHV...PDHDTVTEERDEAWVVGMAI...MSVIVLAIIVFGNVLVITAIKAFERLQITVITNY  
MGSLLQ...PQA...GNA...NGTEAPG...GGARATPYSLQVT...LTLVCLAGLI...MLLTIVFGNVLVITAIKAFERLQITVITNY  
MDVLS...PGQ...QNTTSPAPFE...TCGNTTGISDVTVSQV...ITSLLIGLI...IFCAVIGNAGVVAIAIERSLQNVANY  
MNTSAPPAVSPNITVLAP...GKGPWQVA...SGLDSNATGITAFSMPGWQLALWTAAYLAI...VLVAVMGNATVIWIILAHQRMRIIVITNY  
MGACV...VMTDINIS...SGLDSNATGITAFSMPGWQLALWTAAYLAI...VLVAVMGNATVIWIILAHQRMRIIVITNY

D<sub>6</sub>  
β<sub>6</sub>  
α<sub>6</sub>  
G-21  
M<sub>1</sub>  
SK

II  
LIVSLAMADIIVATLVMPWVVYLEVGEWKF...SRHCDIFVTLDMCTASILNLCAISIQRYTAVAMPIMTRYSSKRR  
FIVSLACADLVMGIAVVPFGASHIIMKMNFGNFWCEFWTSIQVLCVTASIEITLCVIAVQRYIAITSEFKYQSLLTKNKA  
FIVSLASADILVATLVIPFSLANEVQWYEGKTWCEIYALDVLCTSSIVHLCAISIQRYWSITQAIENLKRTPRRI  
LUGSLAVTIDIMVSVLVITEMAALYQVNLNNTLGLQVTCDFIALDVLCTSSIVHLCAISIQRYWSITQAIENLKRTPRRI  
FLLSLACADLIIGFISMNLYTYYLLMQIHWALGTLACDLWLALDYVASNAVNMNLIISFQRYFSVTRPLSRAKTRPRRA  
FIVNLAIDICMAAFNAAFNFVYASHNIWYEGRAFQYFQNLFPITAMFVSJYSMTAIAAQRYMAIVRPFQPRLSAPGTR.

D<sub>6</sub>  
β<sub>6</sub>  
α<sub>6</sub>  
G-21  
M<sub>1</sub>  
SK

V  
VTMIAIIVWVISEITISC...PLLEGLNNTD...QNECIANPAFVVYSSIMSFYVPIVITLLVYIKIYIVLKRKRKRVNTR--(111)  
RMV...ILMVWIVSGLTSFPIQMHWRATH...QKAIIDCYHRETCDFFTNQAYAIWSSIVSVFVPIVIMVVFVYSRVFQVAKRQLQKI--(32)--  
KAI...LITVWVISAIVISFPLISIEKKGG...GGPQPAEPRCEINDQKWYVITSSCIGSFAPQIIMLVYVRIYQIAKRTRVP--(137)  
ALT...SLT...MLIGFLISIPMLGWRTPEDR...SDPDACITISKDMGYTIVSTFGAFYIPILMLVLVYGRIFRAARFIPKT--(110)  
ALM...IGLAWLVSEVLWA...PAILFWQYLVGE...RTVLACQCYIQFLSQPIITFTGTAMAAFYLPVIMCTIYWRIRYRETNAREL--(137)  
AV...IAGIWLVALALAF...PQCFYSTITTDEGATKCVVAWPEDSGGKMLLYHLIVIALIYE...LPVIMFVAVSVIGLTLWRSVPG--(12)--

D<sub>6</sub>  
β<sub>6</sub>  
α<sub>6</sub>  
G-21  
M<sub>1</sub>  
SK

VII  
-KEKKATQMTIAIVIMFIIICWLPFFITHIINIHCOCN...IPFVLYSAFTWLGYNVA...VNP...IYTTIENIEFRMAFMKILHC  
-KEKKALKTIGIMGIFTLWLPFFIVNIVHVIQDNL...IPKEVYILLNLWLGYNVA...PNP...IYCRSP...DFRIAFQEL...CL--(36)  
-REKRTFTVIAVIMGVVVCWEPFFETTYTAVGCS...VPRTEKFFPWEYCNSS...LNP...VLYTLENHDFRRAFMKIL...CRC--(6)  
-REKRTVKTLOIMGIFILCWLPFFIVLVLPPCESSC...HMP...IIGAIINWLGYSNL...INP...VLYAYENKDFQNAFMKILKCNFCRQ  
-KEKKARTLSAILLAFIVTWTINIMVLVSTFCCKDC...VETILWELGYWIGYVNST...LNP...MALQNKAFRDTFRLLHCR--(24)  
-AKKIFVKTMVIVVVTFAICWLPYHLYFIIGTFQEDIYCHKFIQVYLALPWA...MSTMYNP...IYCCINHRFSQERLAPRCC--(62)



9.5 ———  
7.5 ———  
4.4 ———  
2.4 ———  
1.35 ———

FIG. 3

20250303 15:00:00

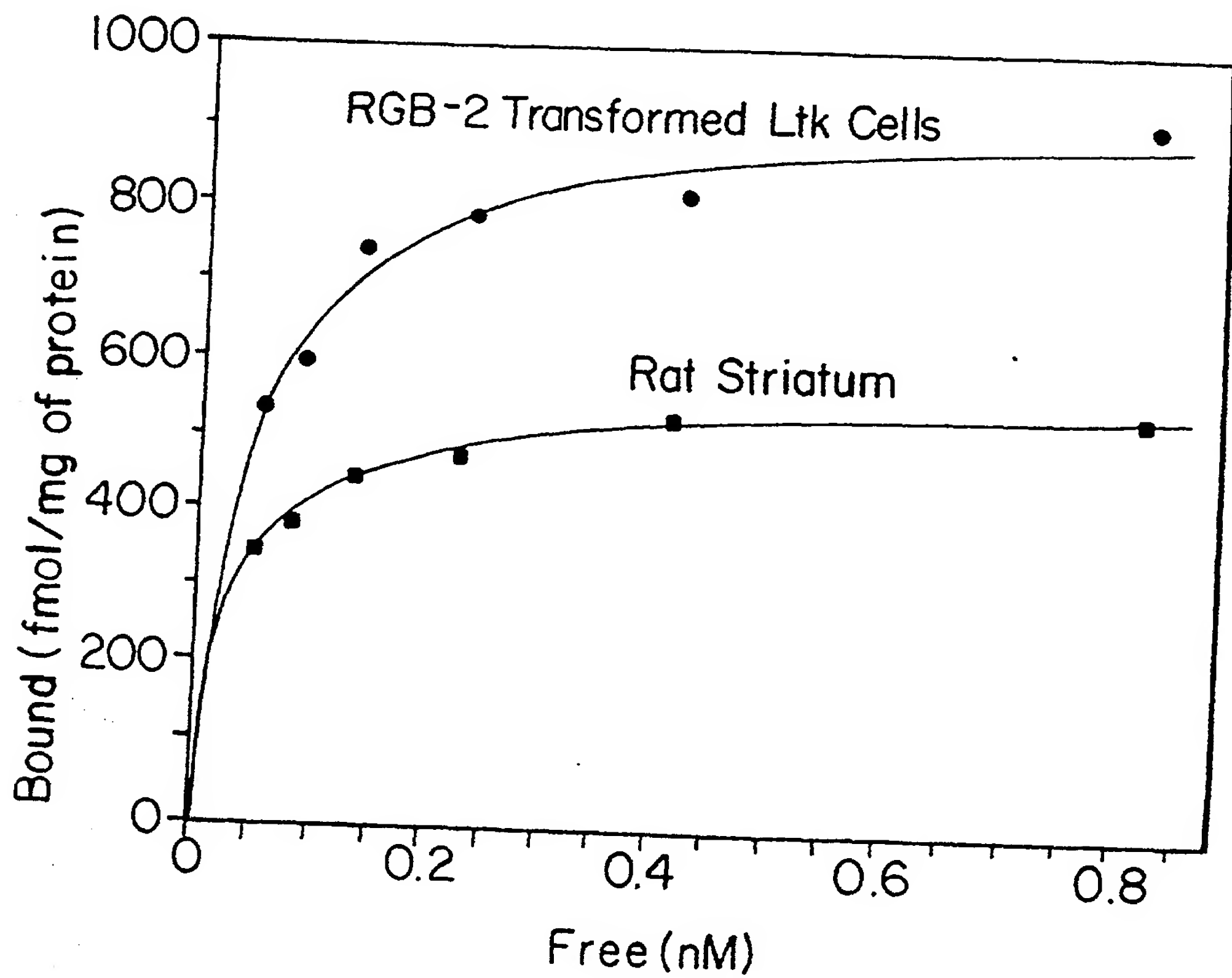


FIG.4A-1

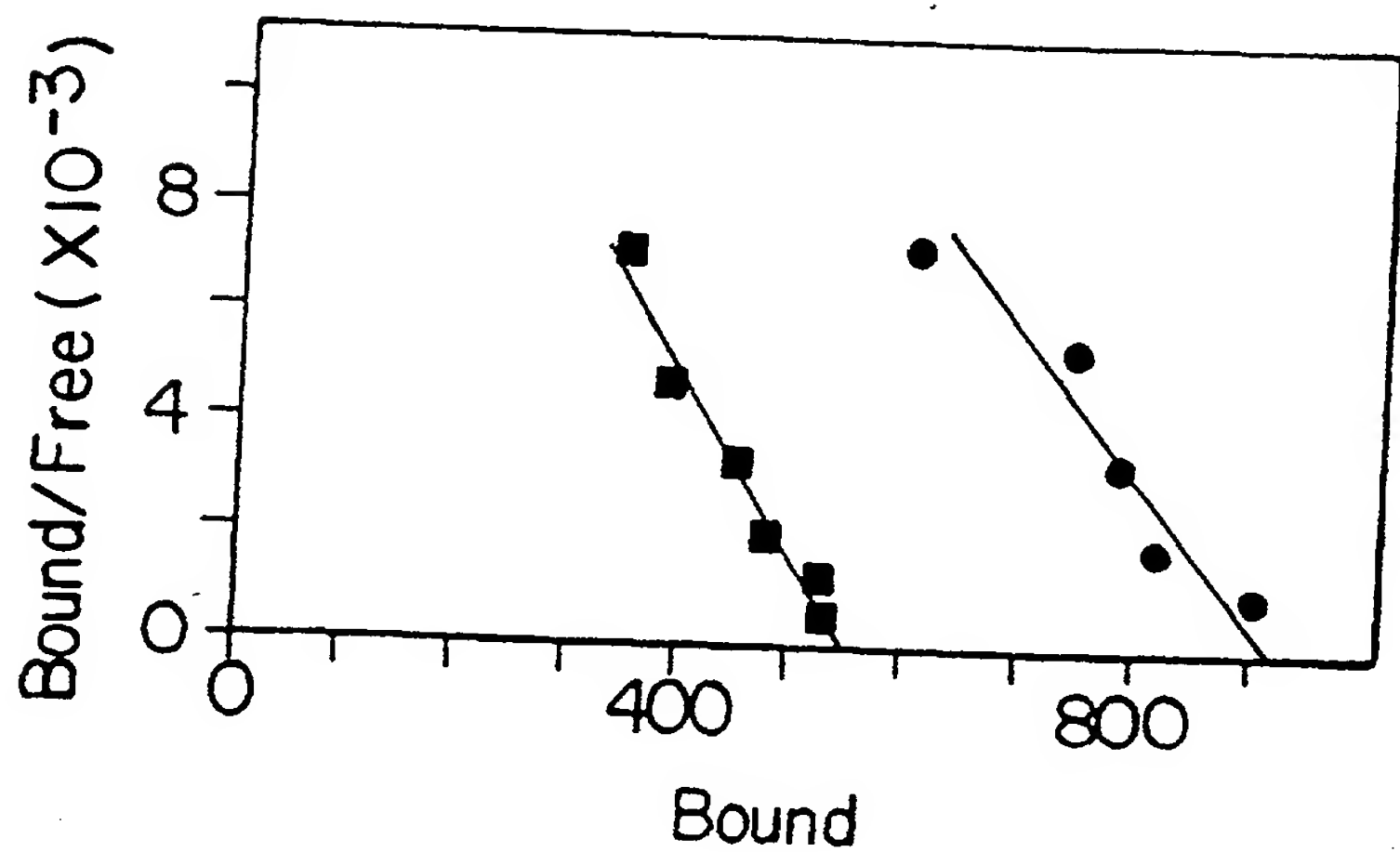


FIG.4A-2



DRUG

Ki (nM)

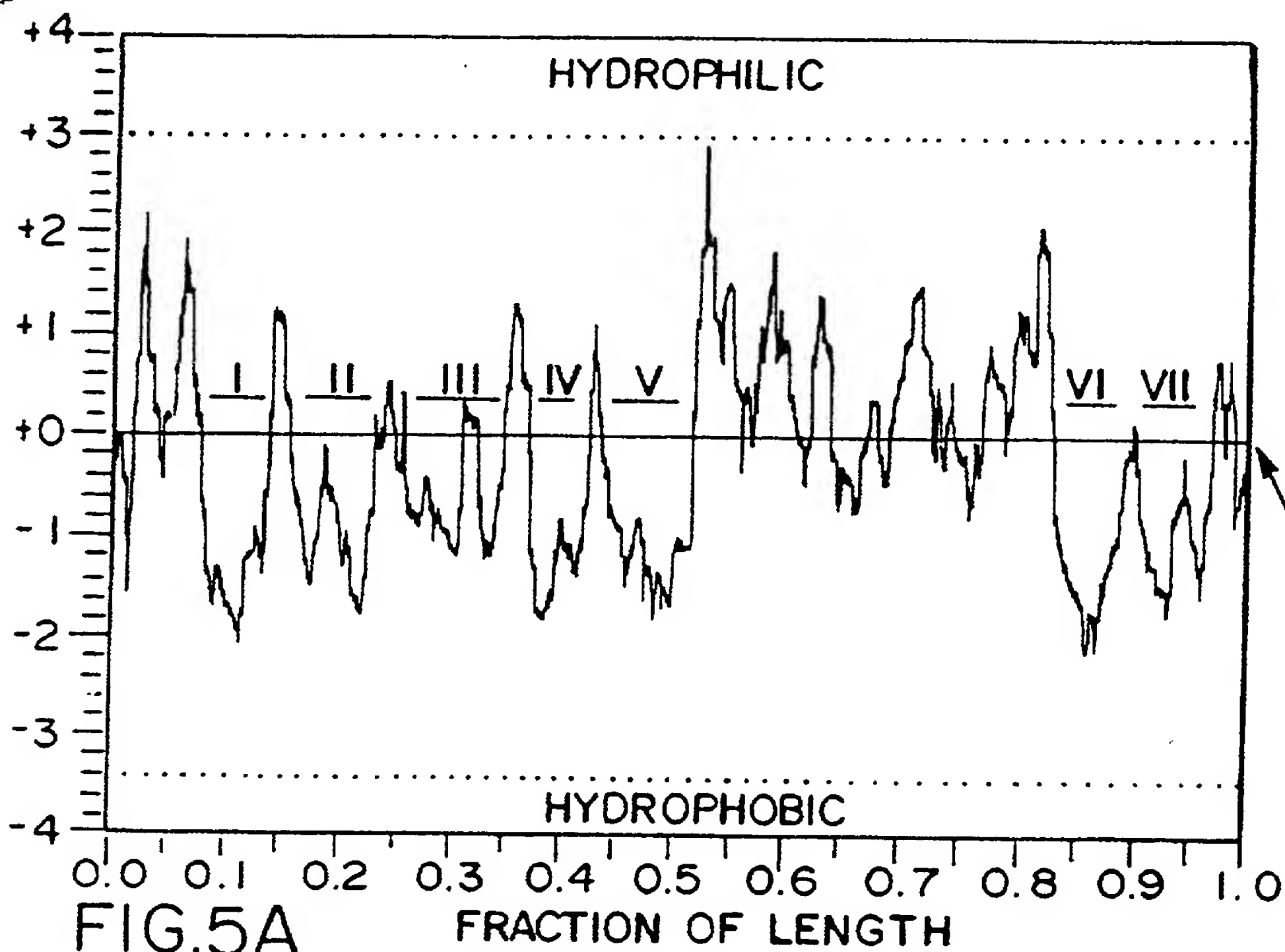
RGB-2

Transformed Ltk-Cells

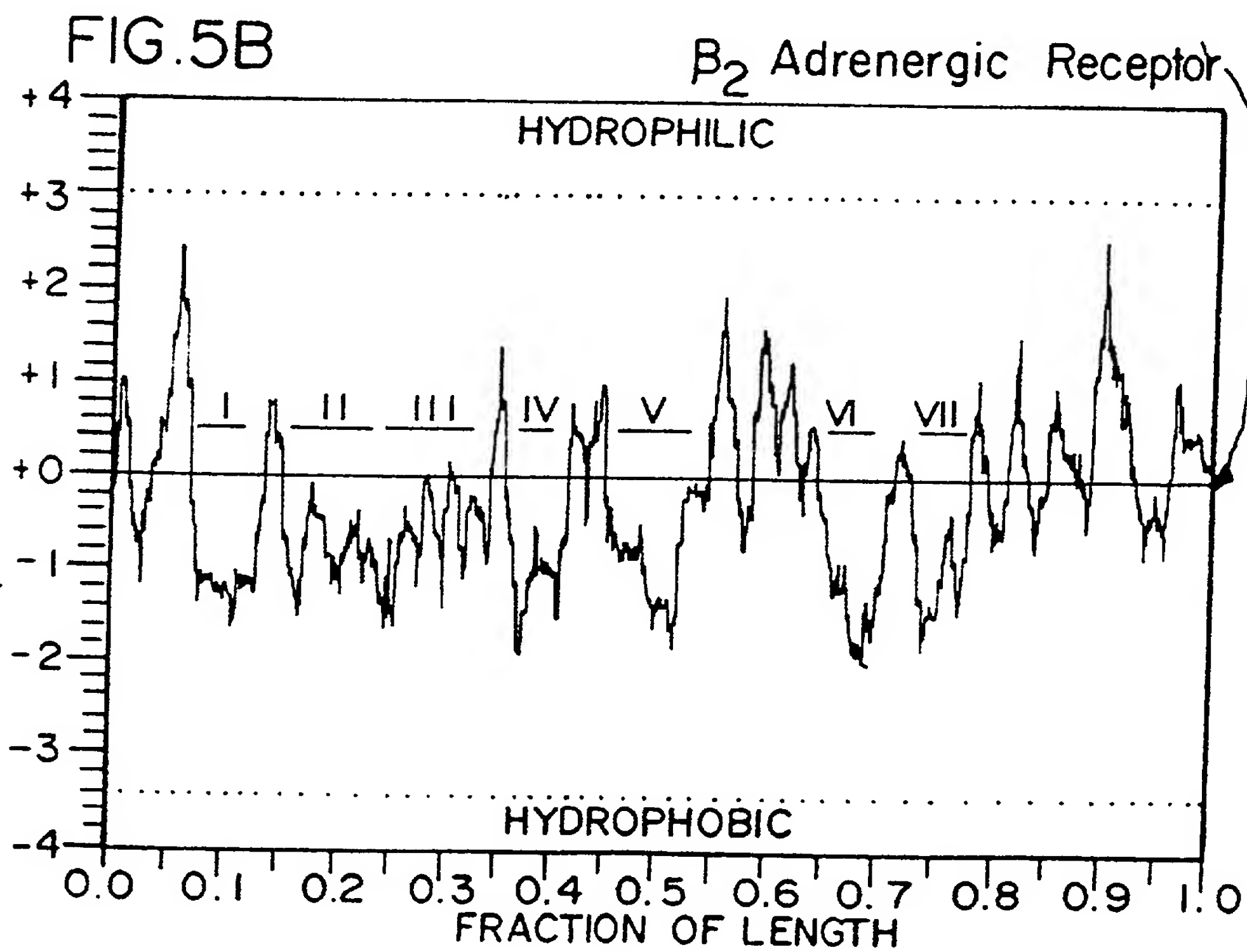
Rat Striatum

|                |        |               |
|----------------|--------|---------------|
| (+)-Butaclamol | 0.83   | 1.0           |
| (-)-Butaclamol | >1,000 | >1,000        |
| Haloperidol    | 3.0    | 5.3           |
| Dopamine + GTP | 17,000 | 6,300         |
| Sulpiride      | 80     | 67 (87%)      |
| high affinity  | ---    | >10,000 (13%) |
| low affinity   | ---    |               |
| SCH 23390      | 1,000  | 35 (16%)      |
| high affinity  | ---    | 780 (84%)     |
| low affinity   | ---    |               |
| Ketanserin     | >1,000 | 27 (25%)      |
| high affinity  | ---    | >1,000 (75%)  |
| low affinity   | ---    |               |

FIG. 4C

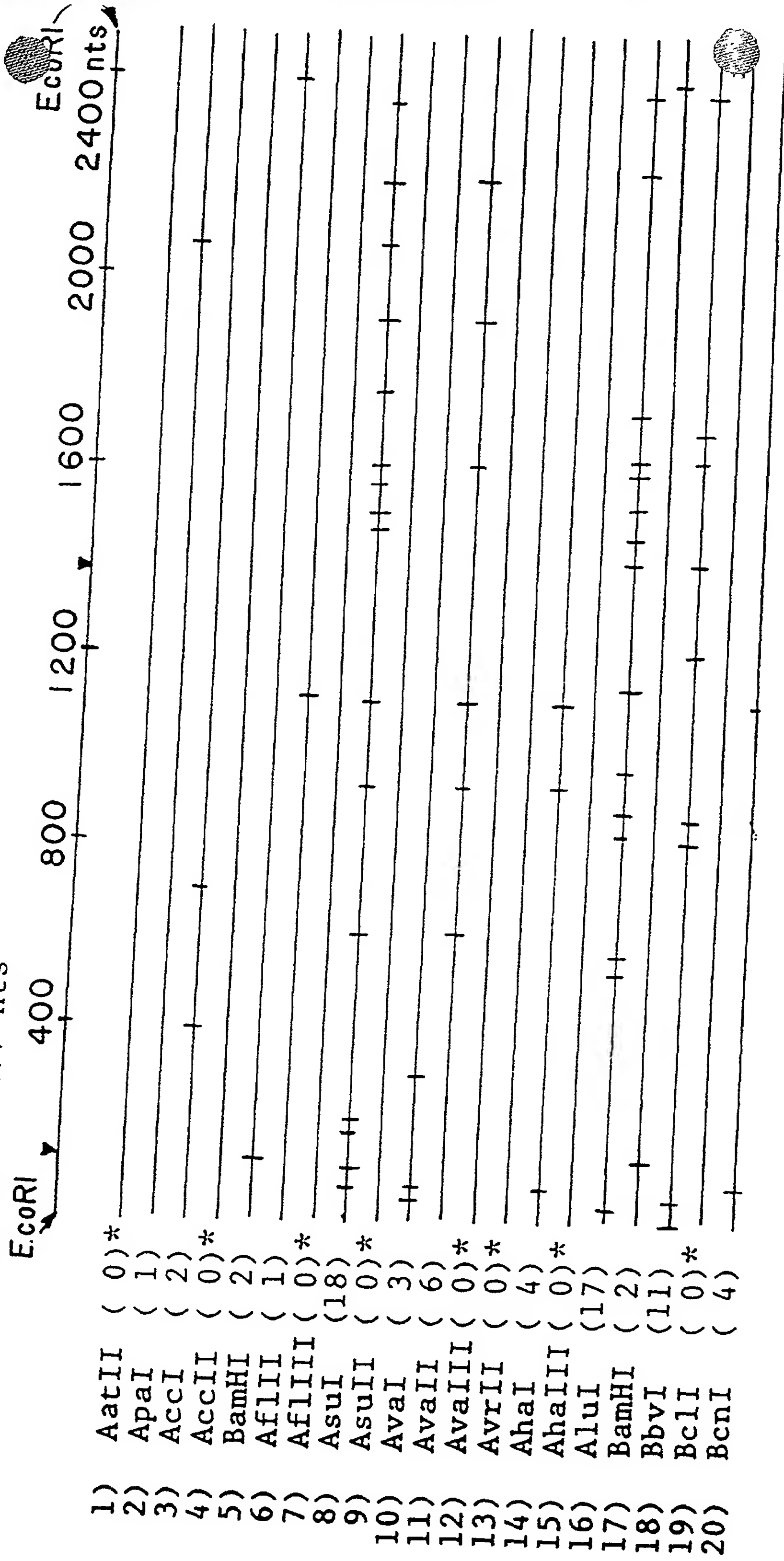


RGB-2



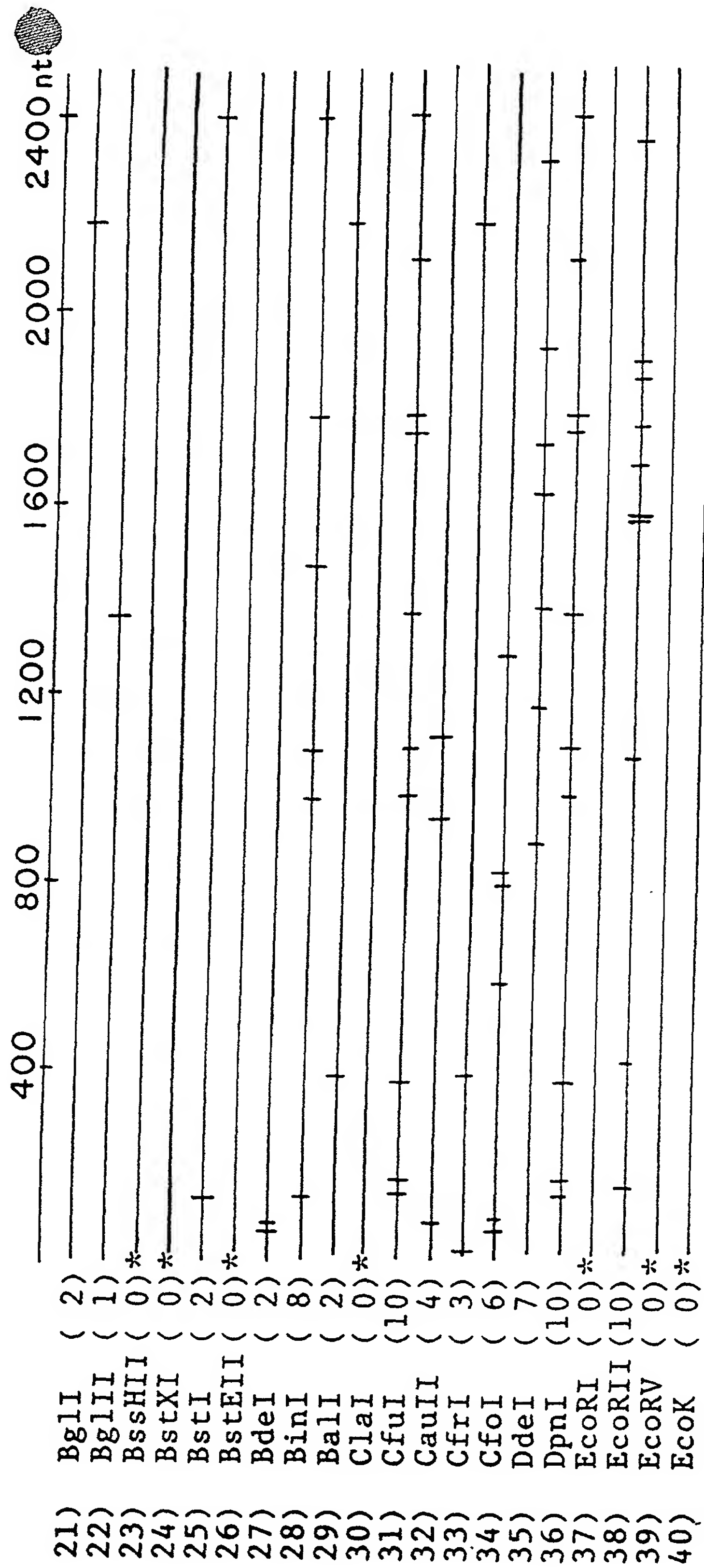
# FIG. 6A

Length of DNA: 2477 nts





| Year | 1970 | 1971 | 1972 | 1973 | 1974 | 1975 | 1976 | 1977 | 1978 | 1979 | 1980 | 1981 | 1982 | 1983 | 1984 | 1985 | 1986 | 1987 | 1988 | 1989 | 1990 | 1991 | 1992 | 1993 | 1994 | 1995 | 1996 | 1997 | 1998 | 1999 | 2000 | 2001 | 2002 | 2003 | 2004 | 2005 | 2006 | 2007 | 2008 | 2009 | 2010 | 2011 | 2012 | 2013 | 2014 | 2015 | 2016 | 2017 | 2018 | 2019 | 2020 | 2021 | 2022 | 2023 | 2024 | 2025 | 2026 | 2027 | 2028 | 2029 | 2030 | 2031 | 2032 | 2033 | 2034 | 2035 | 2036 | 2037 | 2038 | 2039 | 2040 | 2041 | 2042 | 2043 | 2044 | 2045 | 2046 | 2047 | 2048 | 2049 | 2050 | 2051 | 2052 | 2053 | 2054 | 2055 | 2056 | 2057 | 2058 | 2059 | 2060 | 2061 | 2062 | 2063 | 2064 | 2065 | 2066 | 2067 | 2068 | 2069 | 2070 | 2071 | 2072 | 2073 | 2074 | 2075 | 2076 | 2077 | 2078 | 2079 | 2080 | 2081 | 2082 | 2083 | 2084 | 2085 | 2086 | 2087 | 2088 | 2089 | 2090 | 2091 | 2092 | 2093 | 2094 | 2095 | 2096 | 2097 | 2098 | 2099 | 2100 |
|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|
| 1970 | 1971 | 1972 | 1973 | 1974 | 1975 | 1976 | 1977 | 1978 | 1979 | 1980 | 1981 | 1982 | 1983 | 1984 | 1985 | 1986 | 1987 | 1988 | 1989 | 1990 | 1991 | 1992 | 1993 | 1994 | 1995 | 1996 | 1997 | 1998 | 1999 | 2000 | 2001 | 2002 | 2003 | 2004 | 2005 | 2006 | 2007 | 2008 | 2009 | 2010 | 2011 | 2012 | 2013 | 2014 | 2015 | 2016 | 2017 | 2018 | 2019 | 2020 | 2021 | 2022 | 2023 | 2024 | 2025 | 2026 | 2027 | 2028 | 2029 | 2030 | 2031 | 2032 | 2033 | 2034 | 2035 | 2036 | 2037 | 2038 | 2039 | 2040 | 2041 | 2042 | 2043 | 2044 | 2045 | 2046 | 2047 | 2048 | 2049 | 2050 | 2051 | 2052 | 2053 | 2054 | 2055 | 2056 | 2057 | 2058 | 2059 | 2060 | 2061 | 2062 | 2063 | 2064 | 2065 | 2066 | 2067 | 2068 | 2069 | 2070 | 2071 | 2072 | 2073 | 2074 | 2075 | 2076 | 2077 | 2078 | 2079 | 2080 | 2081 | 2082 | 2083 | 2084 | 2085 | 2086 | 2087 | 2088 | 2089 | 2090 | 2091 | 2092 | 2093 | 2094 | 2095 | 2096 | 2097 | 2098 | 2099 | 2100 |      |



**FIG. 6B**

235 277 303 329 355 381 407 433 459 485 511 537 563 589 615 641 667 693 719 745 771 797 823 849 875 901 927 953 979 1005 1031 1057 1083 1109 1135 1161 1187 1213 1239 1265 1291 1317 1343 1369 1395 1421 1447 1473 1499 1525 1551 1577 1603 1629 1655 1681 1707 1733 1759 1785 1811 1837 1863 1889 1915 1941 1967 1993 2019 2045 2071 2097 2123 2149 2175 2201 2227 2253 2279 2305 2331 2357 2383 2409 2435 2461 2487 2513 2539 2565 2591 2617 2643 2669 2695 2721 2747 2773 2799 2825 2851 2877 2903 2929 2955 2981 3007 3033 3059 3085 3111 3137 3163 3189 3215 3241 3267 3293 3319 3345 3371 3397 3423 3449 3475 3501 3527 3553 3579 3605 3631 3657 3683 3709 3735 3761 3787 3813 3839 3865 3891 3917 3943 3969 3995 4021 4047 4073 4099 4125 4151 4177 4203 4229 4255 4281 4307 4333 4359 4385 4411 4437 4463 4489 4515 4541 4567 4593 4619 4645 4671 4697 4723 4749 4775 4801 4827 4853 4879 4905 4931 4957 4983 5009 5035 5061 5087 5113 5139 5165 5191 5217 5243 5269 5295 5321 5347 5373 5399 5425 5451 5477 5503 5529 5555 5581 5607 5633 5659 5685 5711 5737 5763 5789 5815 5841 5867 5893 5919 5945 5971 5997 6023 6049 6075 6101 6127 6153 6179 6205 6231 6257 6283 6309 6335 6361 6387 6413 6439 6465 6491 6517 6543 6569 6595 6621 6647 6673 6699 6725 6751 6777 6803 6829 6855 6881 6907 6933 6959 6985 7011 7037 7063 7089 7115 7141 7167 7193 7219 7245 7271 7297 7323 7349 7375 7401 7427 7453 7479 7505 7531 7557 7583 7609 7635 7661 7687 7713 7739 7765 7791 7817 7843 7869 7895 7921 7947 7973 7999 8025 8051 8077 8103 8129 8155 8181 8207 8233 8259 8285 8311 8337 8363 8389 8415 8441 8467 8493 8519 8545 8571 8597 8623 8649 8675 8701 8727 8753 8779 8805 8831 8857 8883 8909 8935 8961 8987 9013 9039 9065 9091 9117 9143 9169 9195 9221 9247 9273 9299 9325 9351 9377 9403 9429 9455 9481 9507 9533 9559 9585 9611 9637 9663 9689 9715 9741 9767 9793 9819 9845 9871 9897 9923 9949 9975 10001

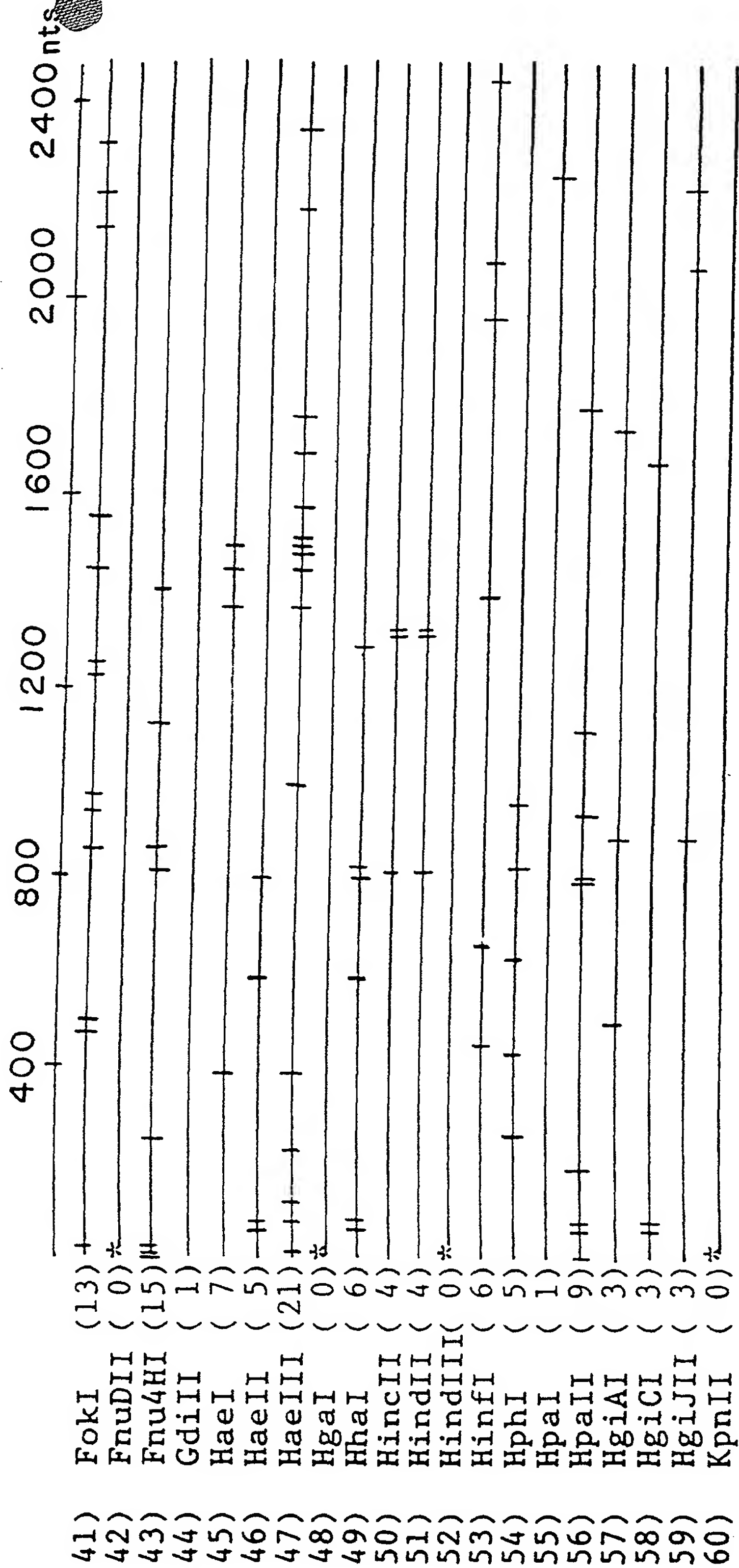


FIG. 6C

61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80

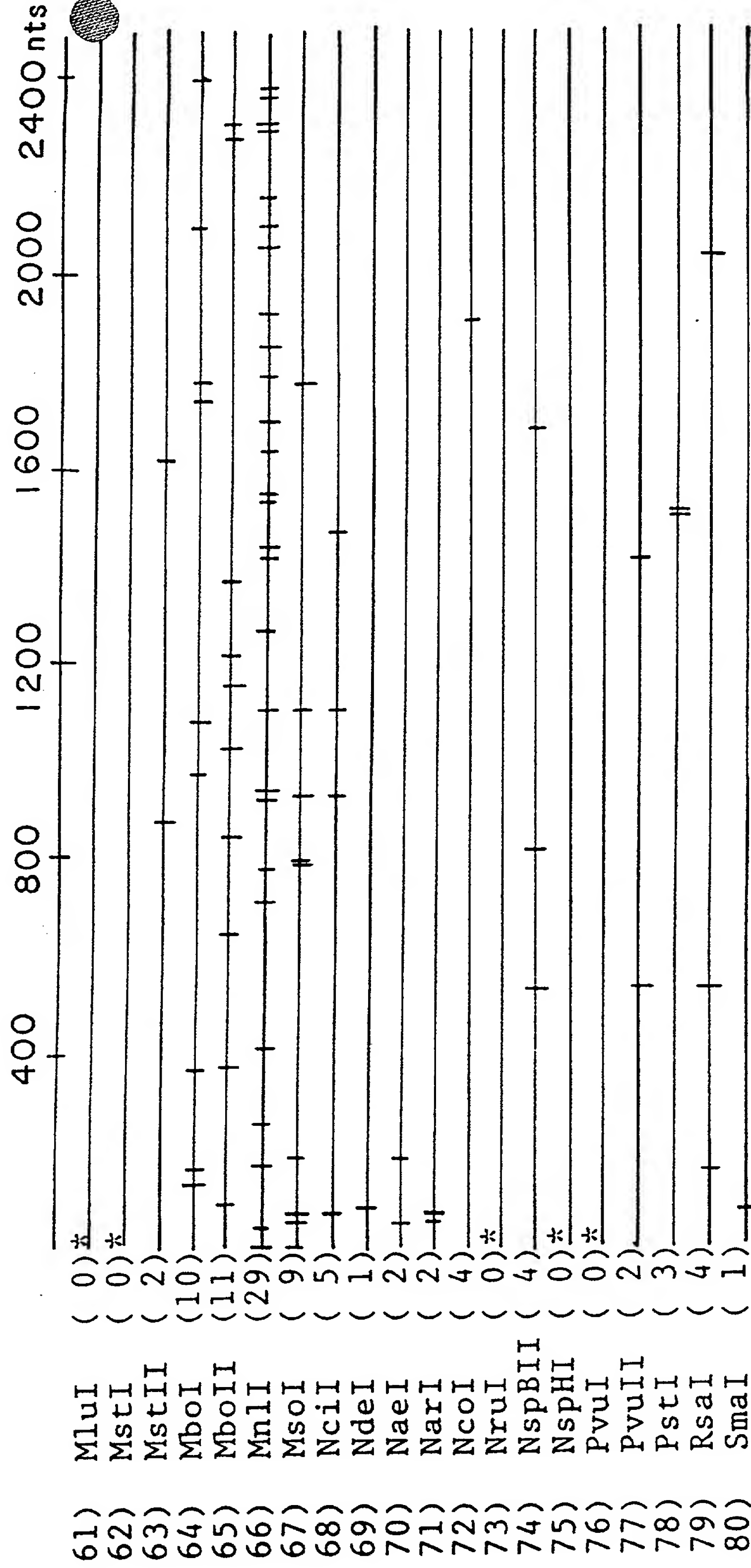


FIG. 6D

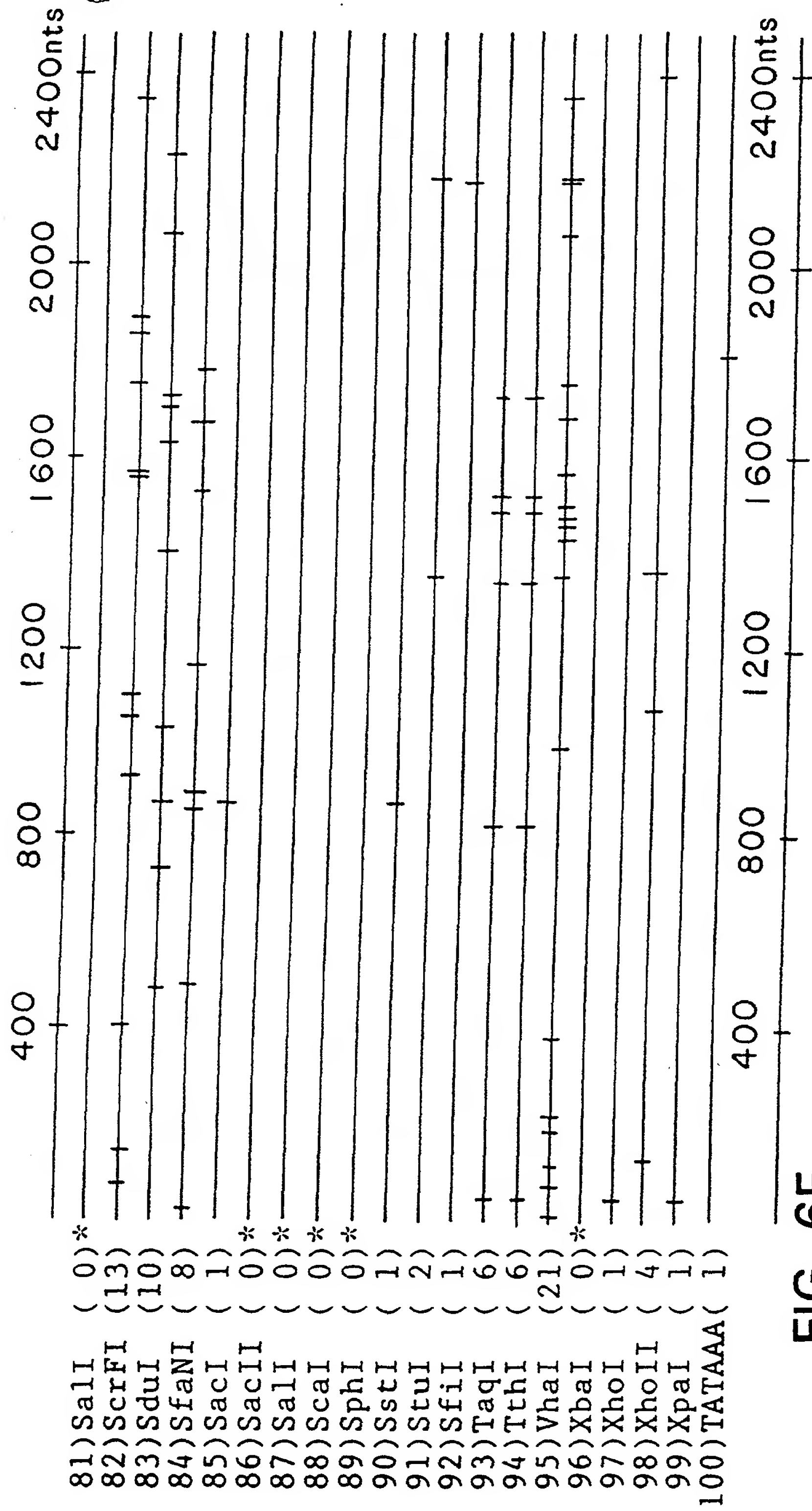


FIG. 6E

FIG. 7A

3' GTC GGG TGG GCT CTC CTG GGC CAT GTC GGG GTA GGG TGG GTC GGT GGT CGA 5' 54  
 5' CAG CCC ACC CGA GAG GAC CCG GCA GTA CAG CCC CAT CCC ACC CAG CCA CCA GCT 3' 54  
 Gln Pro Thr Arg Glu Asp Pro Val Gln Pro His Pro Thr Gln Pro Pro Pro Ala  
 Ser Pro Pro Glu Arg Thr Arg Tyr Ser Pro Ile Pro Pro Ser His His Gln Leu  
 Ala His Pro Arg Gly Pro Gly Thr Ala Pro Ser His Pro Ala Thr Thr Ser

81 108  
 CTG AGA GGG GCT GGG CAG GGT GGT ACC AGA GGT GTC GTG AGG GCT GTC GGG GCG  
 GAC TCT CCC CGA CCC GTC CCA CCA TGG TCT CCA CAG CAC TCC CGA CAG CCC CGC  
 Asp Ser Pro Arg Pro Val Pro Pro Trp Ser Pro Gln His Ser Arg Gln Pro Arg  
 Thr Leu Pro Asp Pro Ser His His Gly Leu His Ser Thr Pro Asp Ser Pro Ala  
 Leu Ser Pro Thr Arg Pro Thr MET Val Ser Thr Ala Leu Pro Thr Ala Pro Pro

135 162  
 GTT TGG TCT CTT CTT ACC CGT ACG GTT TTC CTG GTG GGG TTC CTA ACG GTT CTA  
 CAA ACC AGA GAA GAA TGG GCA TGC CAA AAG GAC CAC CCC AAG GAT TGC CAA GAT  
 Gln Thr Arg Glu Glu Trp Ala Cys Gln Lys Asp His Pro Lys Asp Cys Gln Asp  
 Lys Pro Glu Lys Asn Gly His Ala Lys Arg Thr Thr Pro Arg Ile Ala Lys Ile  
 Asn Gln Arg Arg MET Gly MET Pro Lys Gly Pro Pro Gln Gly Leu Pro Arg Ser

189 216  
 GAA ACT CTA GGT CTG GTA CGG GTT ACC GTT TTG GGC CTG GAG GGA GTT CTG GTA  
 CTT TGA GAT CCA GAC CAT GCC CAA TGG CAA AAC CCG GAC CTC CCT CAA GAC CAT  
 Leu . Asp Pro Asp His Ala Gln Trp Gln Asn Pro Asp Leu Pro Gln Asp His  
 Phe Glu Ile Gln Thr MET Pro Asn Gly Lys Thr Arg Thr Ser Leu Lys Thr MET

**FIG. 7B**

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| CTC | GGC | ATC | CTT | C6A | G55 | GGT | CGT | CTT | CCT | CTT | CTT | TCG | GTG | AGT | CTA | CGA | GCG | 270 |
| GAG | CCG | TAG | GAA | G3T | C44 | CCA | GCA | GAA | GGA | GAA | GAA | AGC | CAC | TCA | GAT | GCT | CGC |     |
| Glu | Pro | .   | Glu | C   | TT  | Pro | Ala | Glu | Gly | Glu | Glu | Ser | His | Ser | Asp | Ala | Arg |     |
| Ser | Arg | Arg | Lys | Leu | Phe | Gln | Gln | Lys | Glu | Lys | Lys | Ala | Thr | Gln | MET | Leu | Ala |     |
| Ala | Val | Gly | Ser |     |     | Ser | Arg | Arg | Arg | Arg | Lys | Pro | Leu | Arg | Cys | Ser | Pro |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| GTA | 5CA | AGA | GCC | GCA | CAA | GTA | GTA | GAC | GAC | CGG | GAA | GAA | GTA | GTG | TGT | GTA | 324 |
| CAT | 4GT | TCT | CGG | CGT | GTT | CAT | CAT | CTG | CTG | GCT | CTT | CTT | CAT | CAC | ACA | CAT |     |
| His | T   | Ser | Arg | Arg | Val | His | His | Leu | Leu | Ala | Ala | Leu | Leu | His | Thr | His |     |
| ILE | Val | Leu | Gly | Val | Phe | Ile | Ile | Cys | Trp | Leu | Pro | Phe | Phe | Ile | Thr | His |     |
| le  | Phe | Ser | Ala | Cys | Ser | Ser | Ser | Ala | Gly | Cys | Pro | Ser | Ser | His | Thr | Ser |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| GGA | CTT | GTA | TGT | GAC | ACT | GAC | GTT | GTA | GGG | CGG | ACA | GGA | CAT | GTC | GCG | GAA | GTG | 378 |
| CCT | GAA | CAT | ACA | CTG | TGA | CTG | CAA | CAT | CCC | GCC | TGT | CCT | GTA | CAG | CGC | CTT | CAC |     |
| Pro | Glu | His | Thr | Leu | .   | Leu | Gln | His | Pro | Ala | Cys | Pro | Val | Gln | Arg | Leu | His |     |
| Leu | Asn | Ile | His | Cys | Asp | Cys | Asn | Ile | Pro | Pro | Val | Leu | Tyr | Ser | Ala | Phe | Thr |     |
| .   | Thr | Tyr | Thr | Val | Thr | Ala | Thr | Ser | Arg | Leu | Ser | Cys | Thr | Ala | Pro | Ser | Arg |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| CAC | CGA | CCC | GAT | ACA | GTT | GTC | GCG | GCA | CTT | GGG | GTA | GTA | GAT | GTG | GTG | GAA | GTT | 432 |
| GTG | GCT | GGG | CTA | TGT | CAA | CAG | CGC | CGT | GAA | CCC | CAT | CAT | CTA | CAC | CAC | CTT | CAA |     |
| Val | Ala | Gly | Leu | Cys | Gln | Gln | Arg | Arg | Glu | Pro | His | His | Leu | His | His | Leu | Gln |     |
| Trp | Leu | Gly | Tyr | Val | Asn | Ser | Ala | Val | Asn | Pro | Ile | Ile | Tyr | Thr | Thr | Phe | Asn |     |
| Gly | Trp | Ala | MET | Ser | Thr | Ala | Pro | .   | Thr | Pro | Ser | Ser | Thr | Pro | Pro | Ser | Thr |     |



459 486  
 GTA ACT CAA GGC GTT CCG GAA GGA CTT CTA GGA GGT GAC GAC TGA GAC GAC GGA  
 CAT TGA GTT CCG CAA GGC CTT CCT GAA GAT CCT CCA CTG CTG ACT CTG CTG CCT  
 His . Val Pro Gln Gly Leu Pro Glu Asp Pro Leu Leu Thr Leu Leu Pro  
 Ile Glu Phe Arg Lys Ala Phe Leu Lys Ile Leu His Cys STOPLeu Cys Cys Leu  
 Leu Ser Ser Ala Arg Pro Ser . Arg Ser Ser Thr Ala Asp Ser Ala Ala Cys

513 540  
 CGG CGT GTC GTC GGA CGA AGG GTG GAG GGA CGG GTC ACG GCC GGT CGG AGT GGG  
 GCC GCA CAG CAG CCT GCT TCC CAC CTC CAC TGC CGG CCA GCC TCA CCC  
 Ala Ala Gln Gln Pro Ala Ser His Leu Pro Ala Gln Cys Arg Pro Ala Ser Pro  
 Pro His Ser Ser Leu Leu Pro Thr Ser Leu Pro Ser Ala Gly Gln Pro His Pro  
 Arg Thr Ala Ala Cys Phe Pro Pro Cys Pro Val Pro Ala Ser Leu Thr Leu

567 594  
 AAC GCT TGG CAC TCG TCC TTC CGG ACC CAC CTA GCC GGA GAA GAT CGG GGC  
 TTG CGA ACC GTG AGC AGG AAG GCC TGG GTG GAT CGG CCT CCT CTA GCC CCG  
 Leu Arg Thr Val Ser Arg Lys Ala Trp Val Asp Arg Pro Pro Leu Leu Ala Pro  
 Cys Glu Pro . Ala Gly Arg Pro Gly Trp Ile Gly Leu Leu Phe . Pro Arg  
 Ala Asn Arg Glu Gln Glu Gly Leu Gly Ser Ala Ser Ser Ser Pro Gly

FIG. 7C

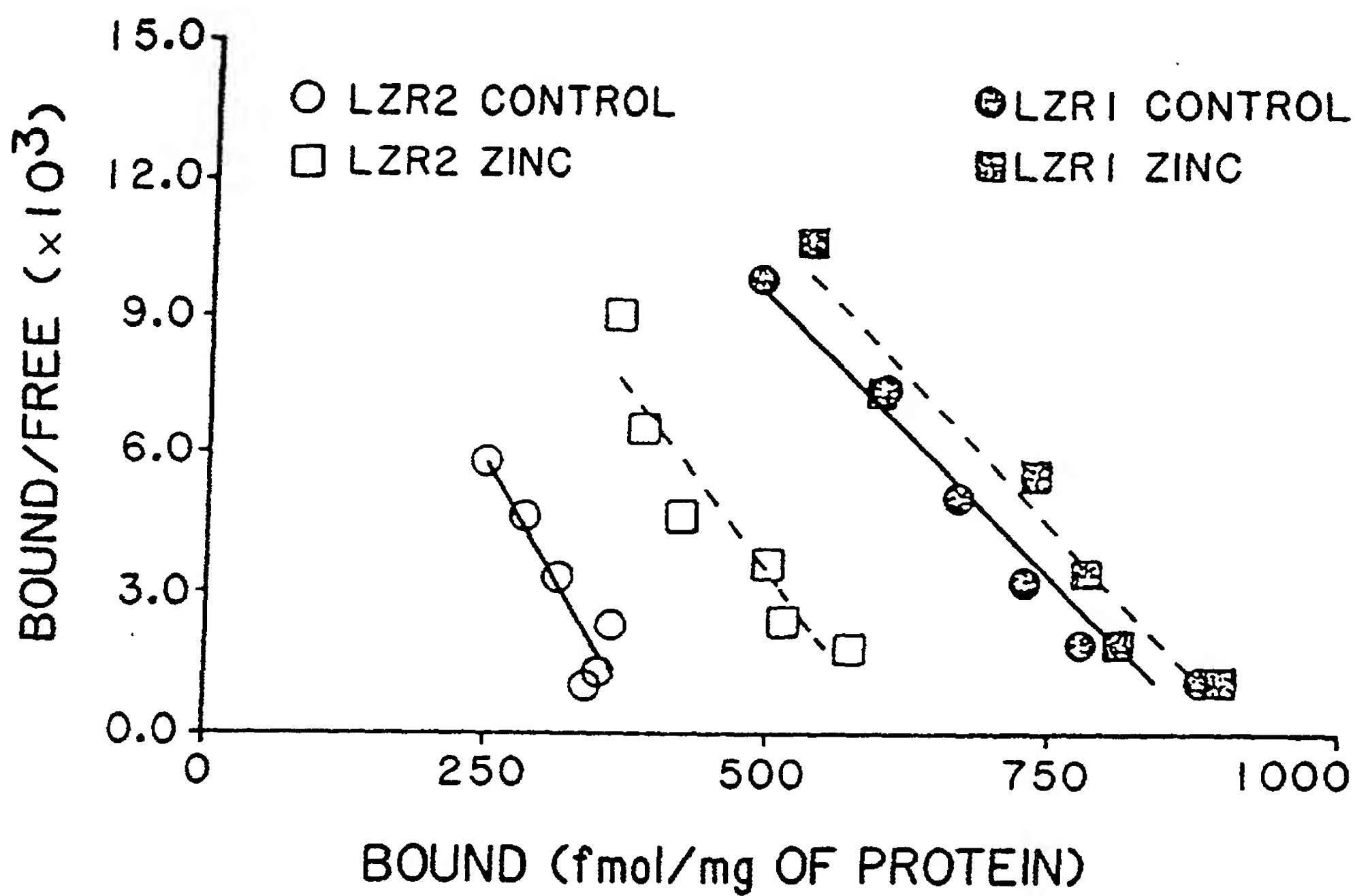


FIG. 8

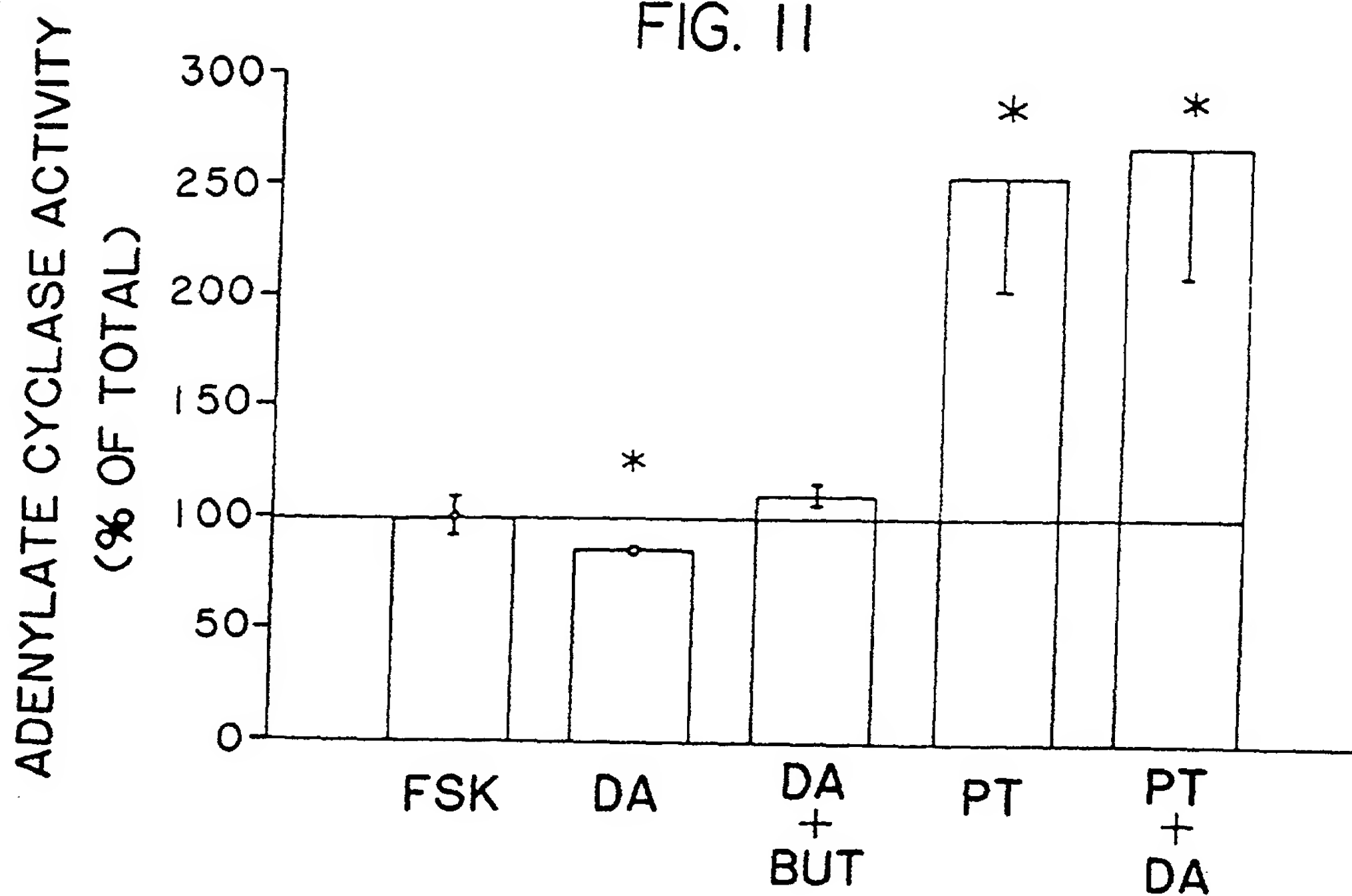


FIG. 9A

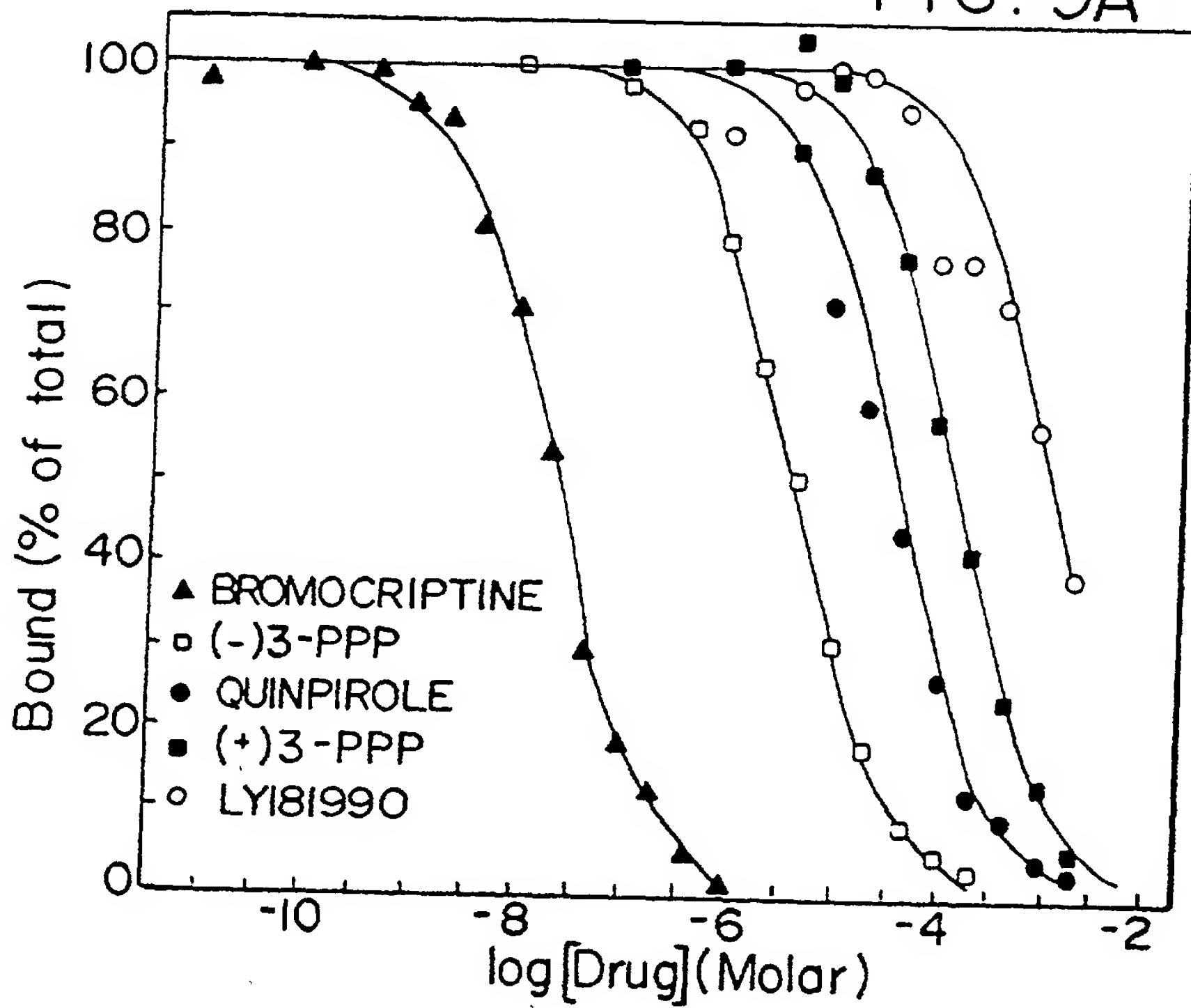
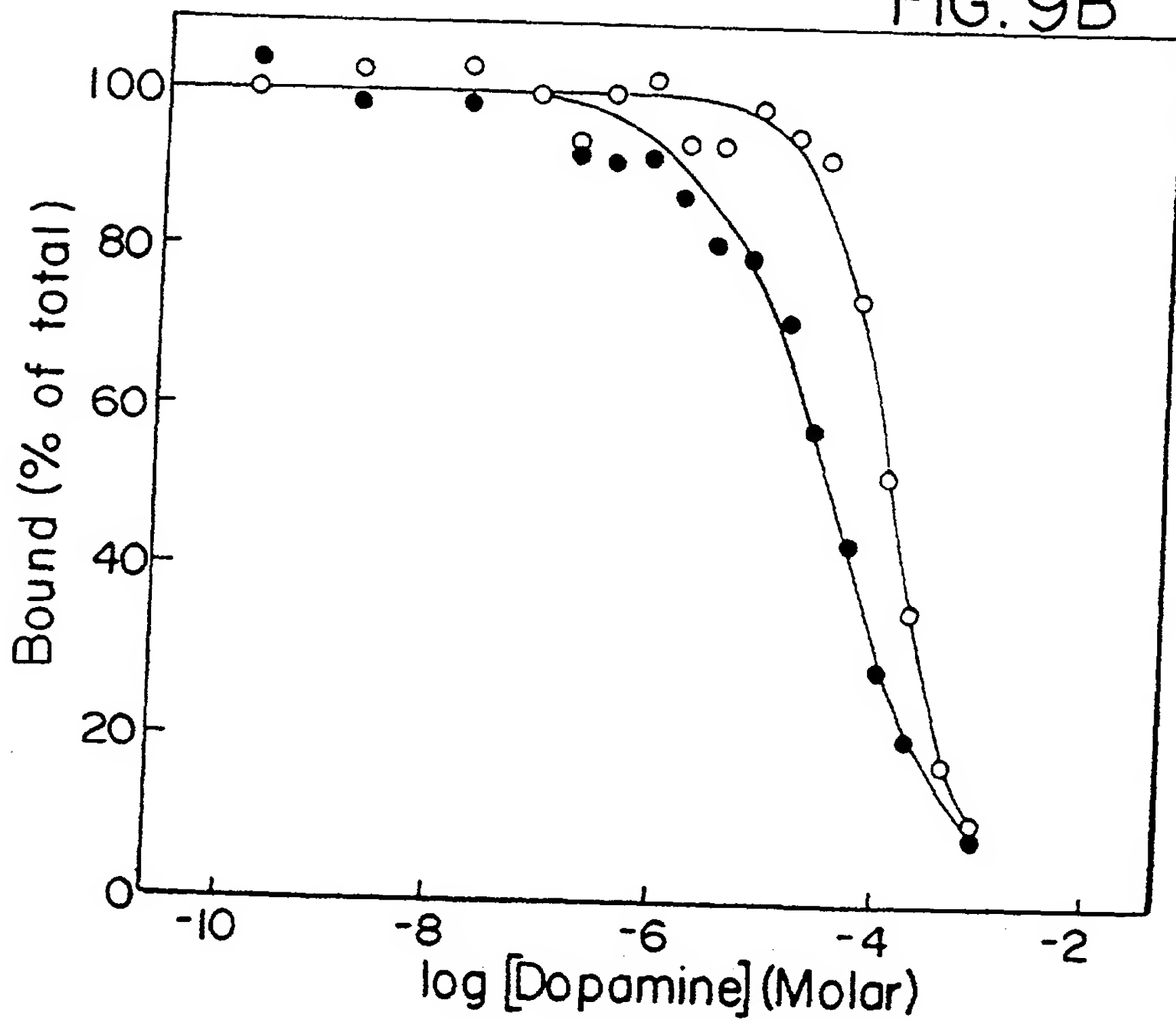


FIG. 9B



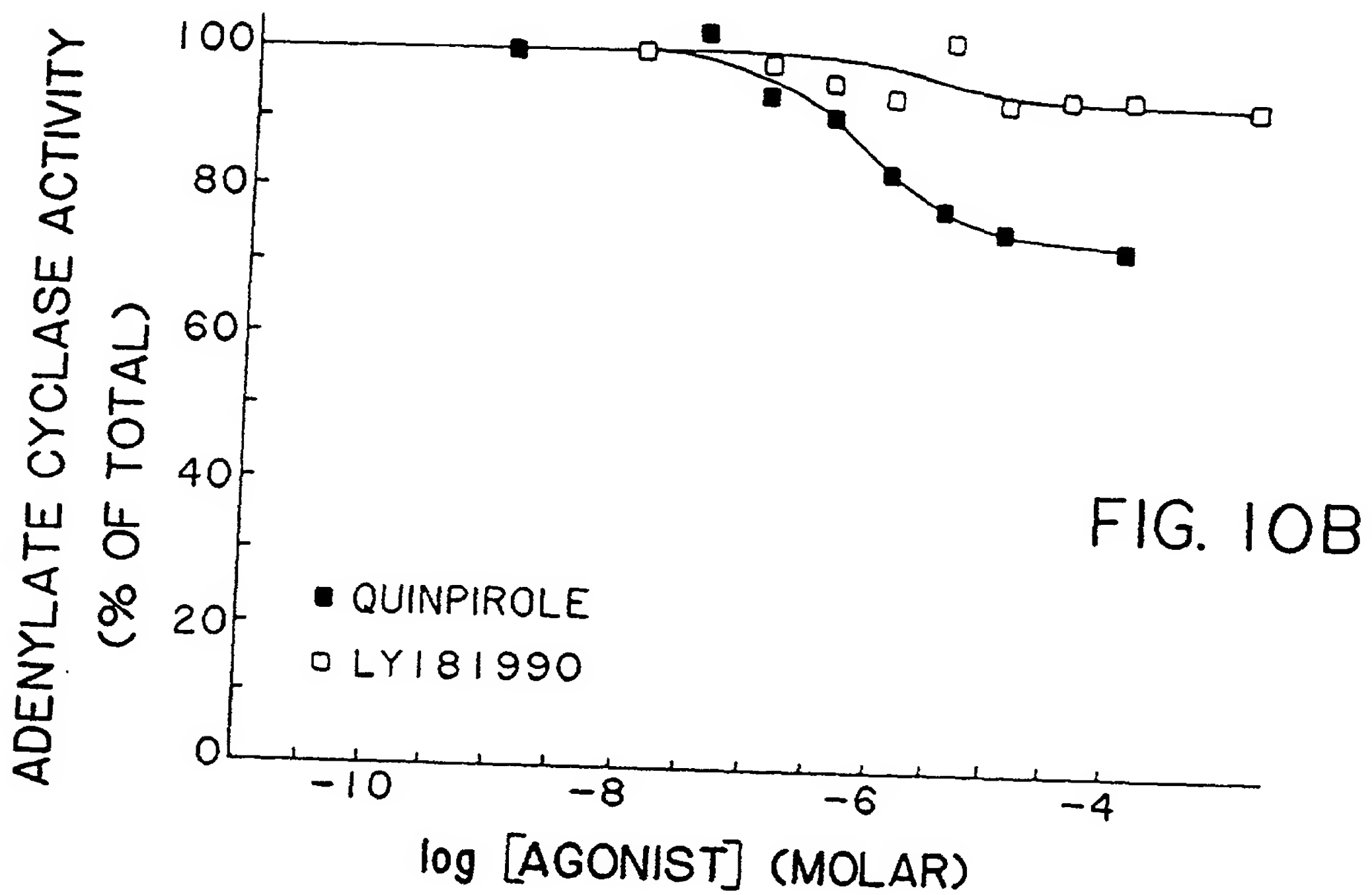
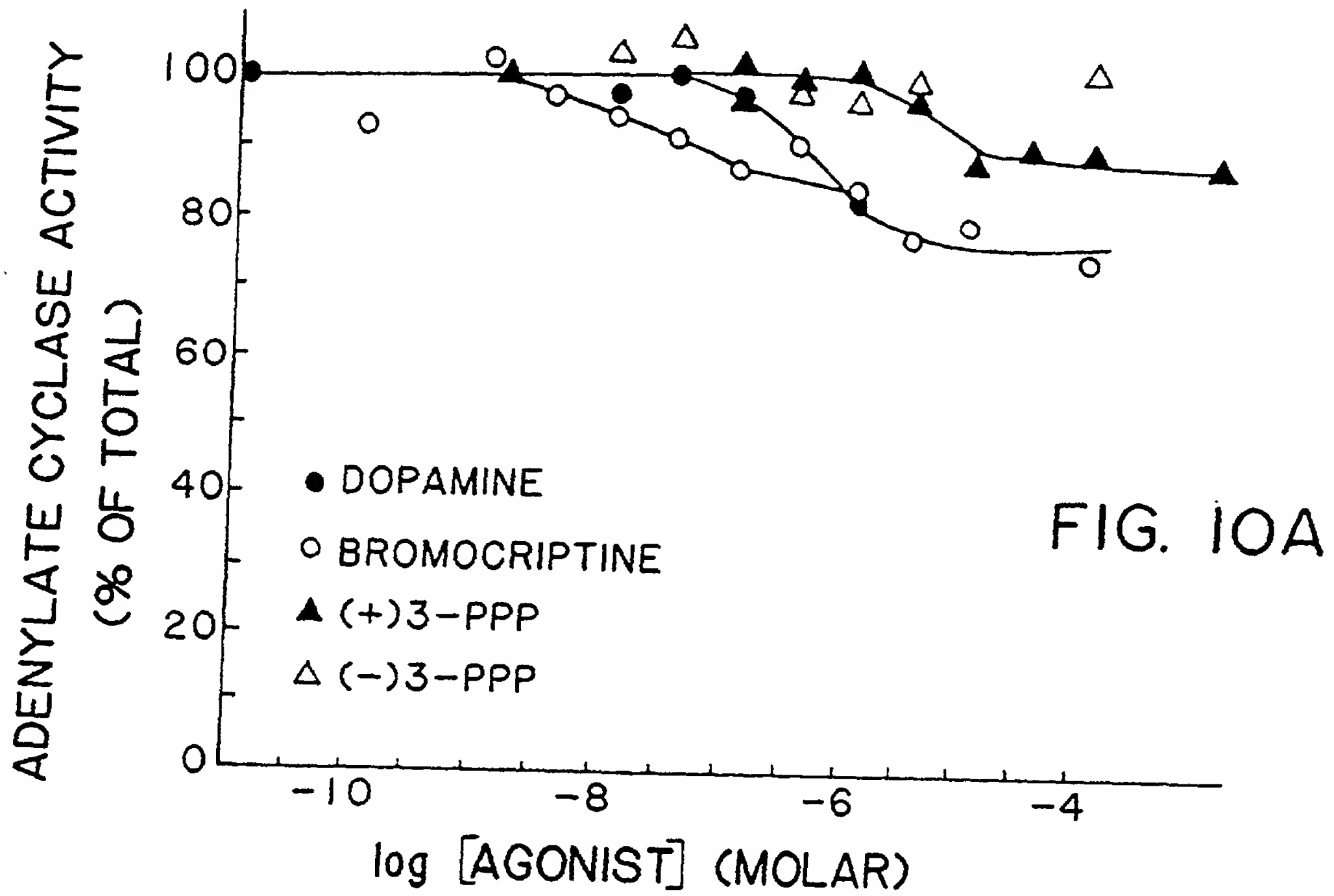


FIG. 12A  
 $\bar{X}$   
S.E.  
INH

| CONTROL |      |        |  | +P.T. |      |        |  |
|---------|------|--------|--|-------|------|--------|--|
| BASAL   | FSK  | FSK+DA |  | BASAL | FSK  | FSK+DA |  |
| 2.1     | 22.6 | 14.3   |  | 1.7   | 26.7 | 23.1   |  |
| 0.2     | 2.2  | 2.1    |  | 0.4   | 2.0  | 0.5    |  |
| —       | —    | 41%    |  | —     | —    | 14%    |  |

FIG. 12B  
 $\bar{X}$   
S.E.  
INH

| CONTROL |      |      |        |  | +P.T. |      |      |        |  |
|---------|------|------|--------|--|-------|------|------|--------|--|
| BASAL   | VIP  | DA   | VIP+DA |  | BASAL | VIP  | DA   | VIP+DA |  |
| 0.60    | 2.41 | 0.32 | 0.84   |  | 0.61  | 2.68 | 0.55 | 2.56   |  |
| 0.02    | 0.31 | 0.02 | 0.13   |  | 0.09  | 0.08 | 0.03 | 0.25   |  |
| —       | —    | 53%  | 71%    |  | —     | —    | 10%  | 3%     |  |

FIG. 12C  
 $\bar{X}$   
S.E.  
INH

| CONTROL |     |      |        |  | +P.T. |      |      |        |  |
|---------|-----|------|--------|--|-------|------|------|--------|--|
| BASAL   | VIP | DA   | VIP+DA |  | BASAL | VIP  | DA   | VIP+DA |  |
| 0.78    | 5.1 | 0.25 | 0.76   |  | 0.64  | 5.29 | 0.66 | 4.76   |  |
| 0.04    | 0.4 | 0.03 | 0.01   |  | 0.01  | 0.44 | 0.03 | 0.16   |  |
| —       | —   | 68%  | 88%    |  | —     | —    | 0%   | 12%    |  |

Figure 1 shows a vertical gel electrophoresis image with four lanes labeled GH4, GH4ZR7, GH4ZR7Zn, and GH4ZD10. On the left side, molecular weight markers are indicated at 9.5, 7.5, 4.4, 2.4, 1.4, and 0.24. The GH4 lane shows a single band at approximately 4.4. The GH4ZR7 lane shows a single band at approximately 2.4. The GH4ZR7Zn lane shows a single band at approximately 2.4. The GH4ZD10 lane shows a single band at approximately 2.4.

FIG. 13A



03540" 55/23333

FIG. 13B-1

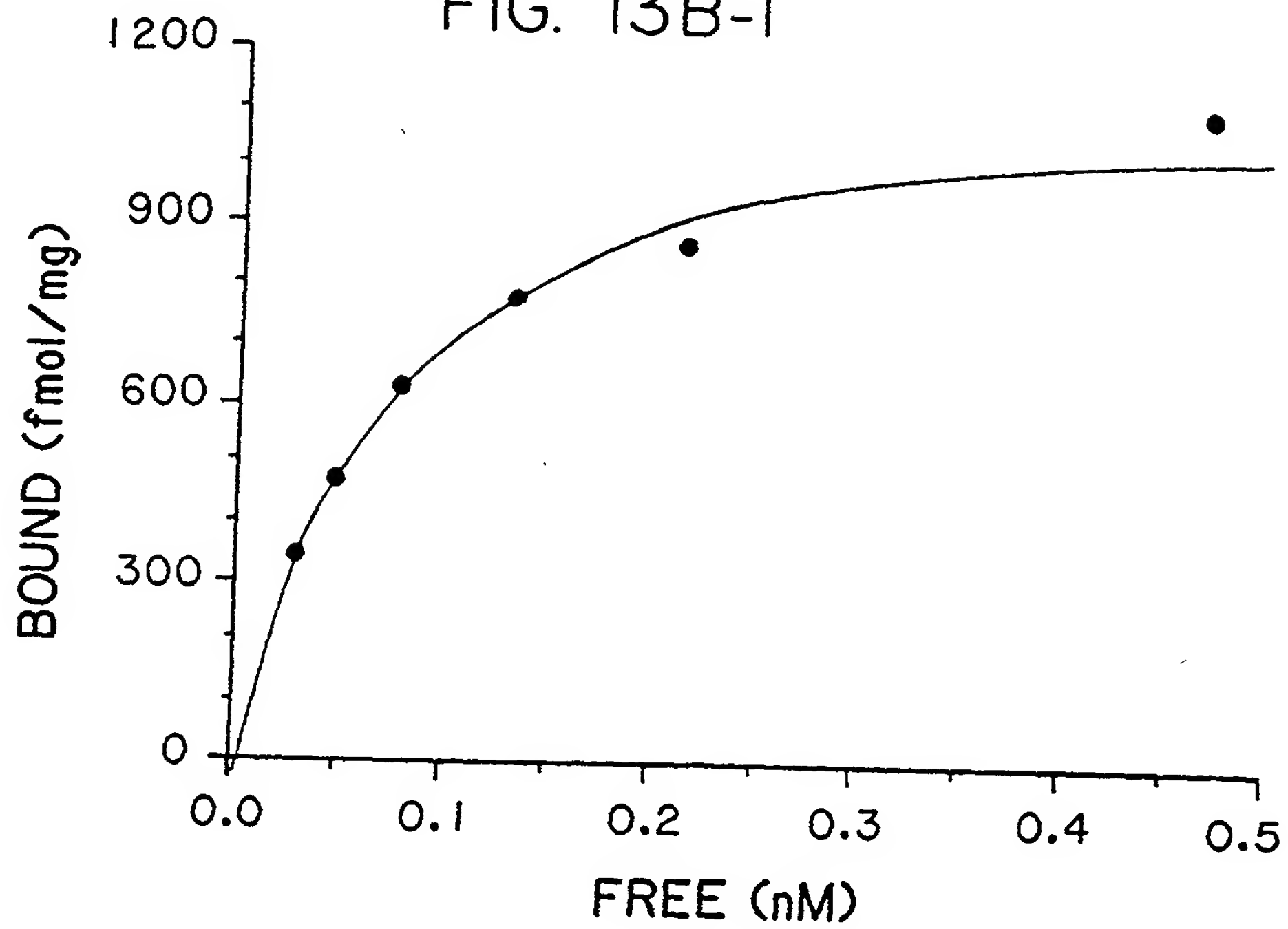
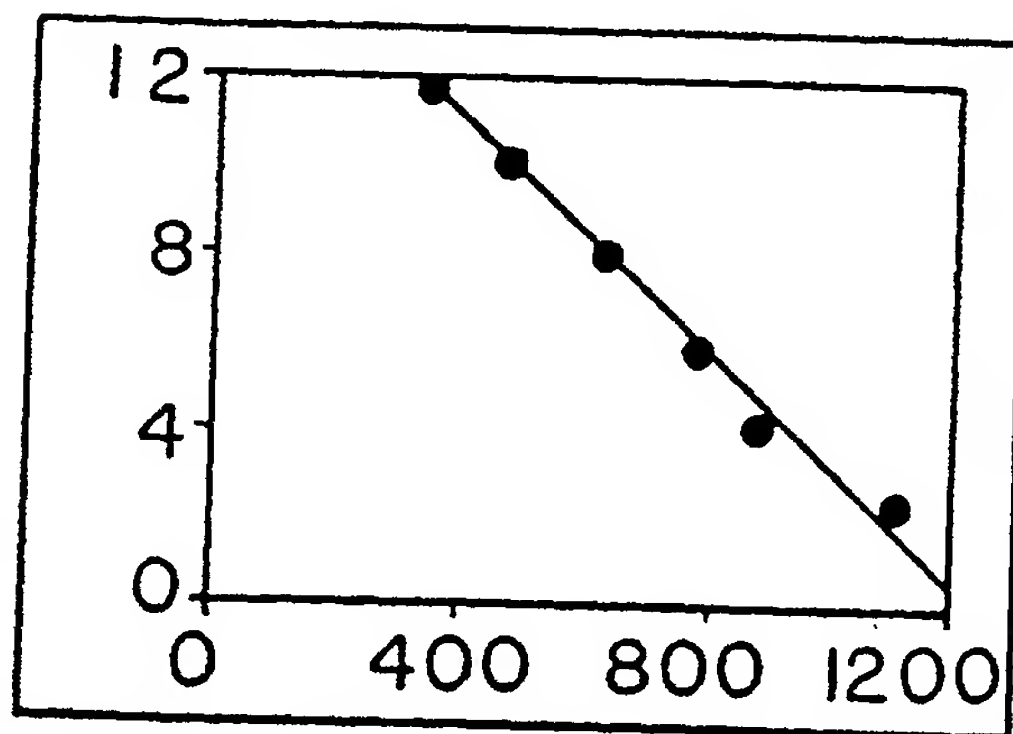


FIG. 13B-2



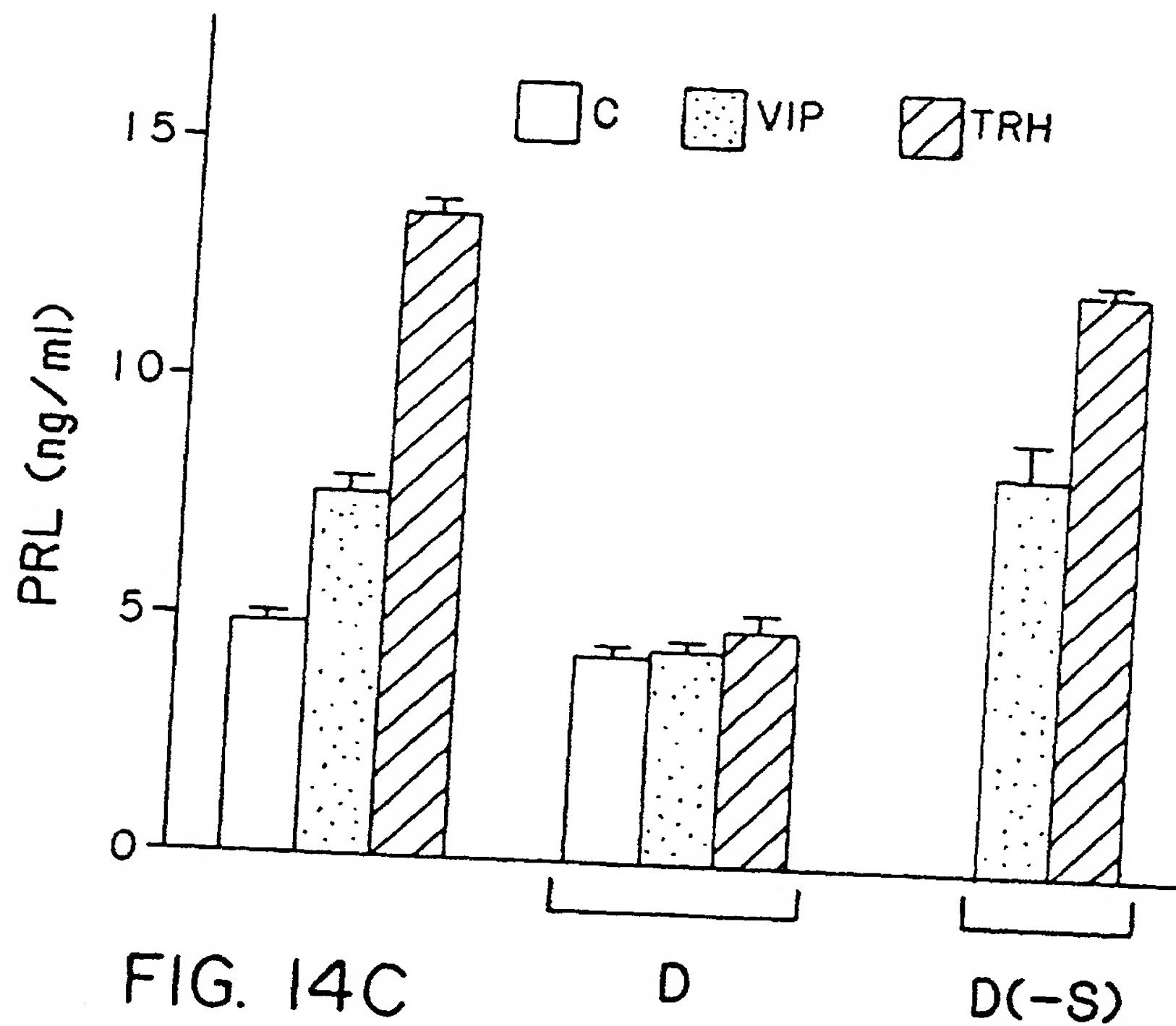
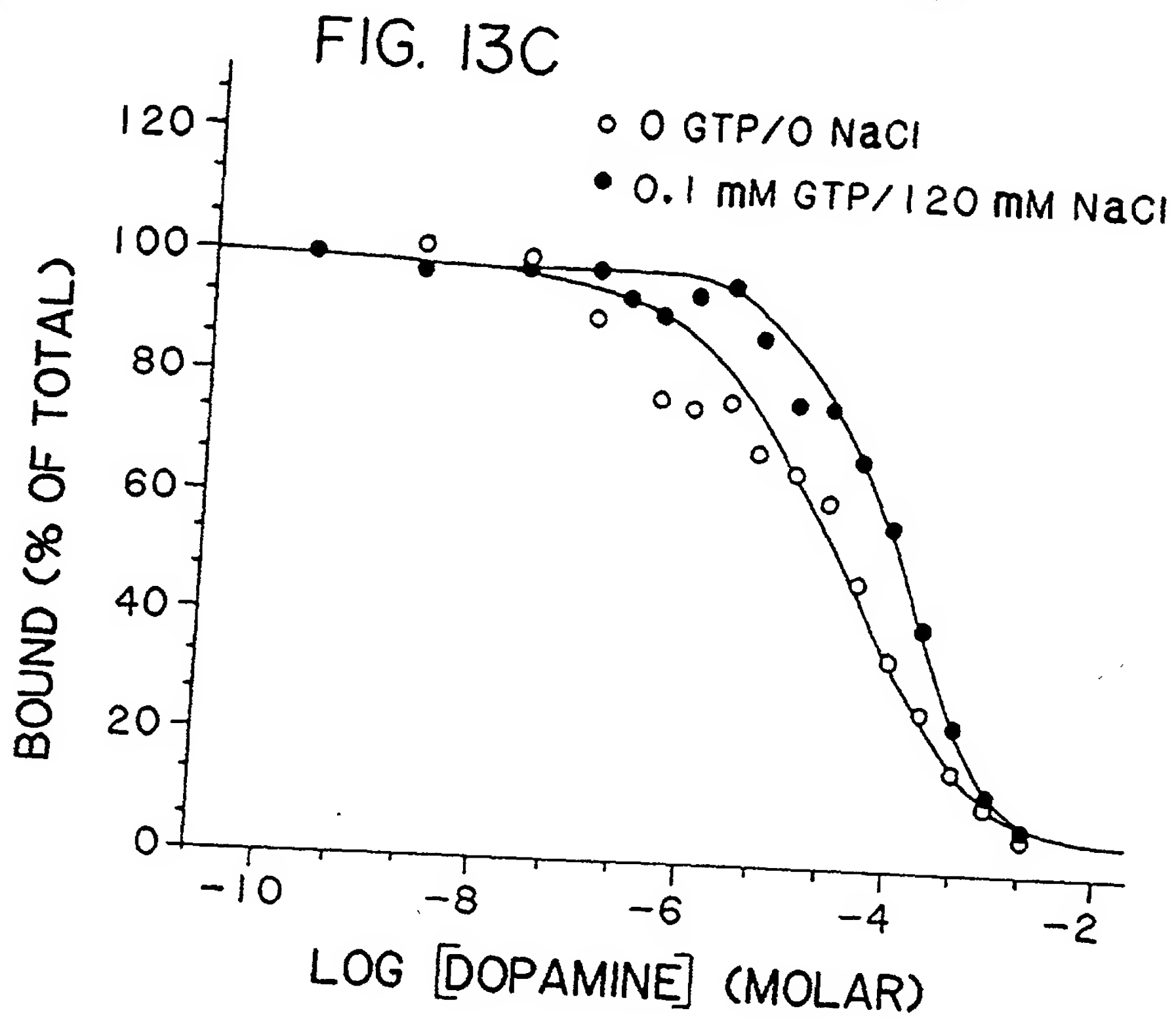


FIG.14A

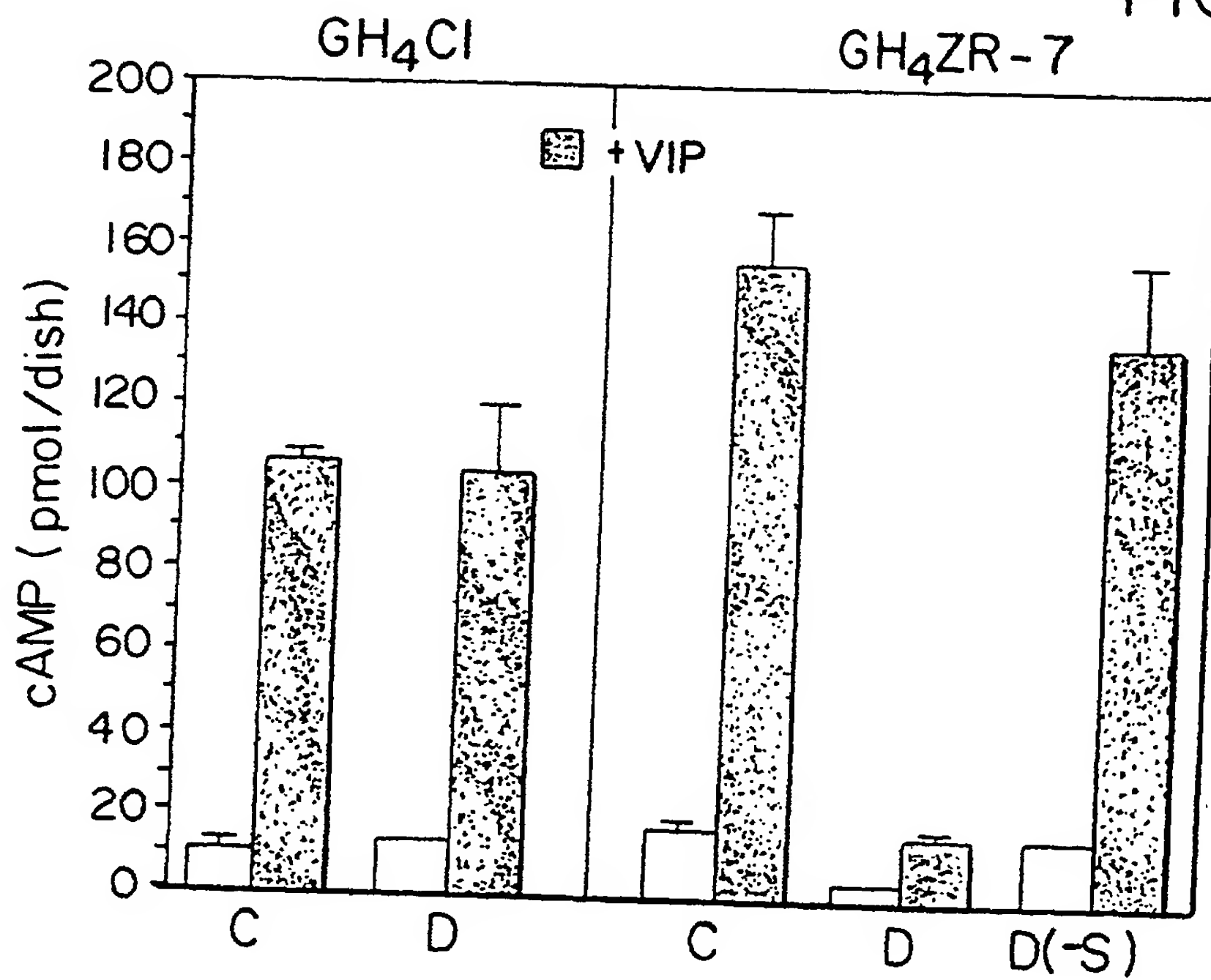
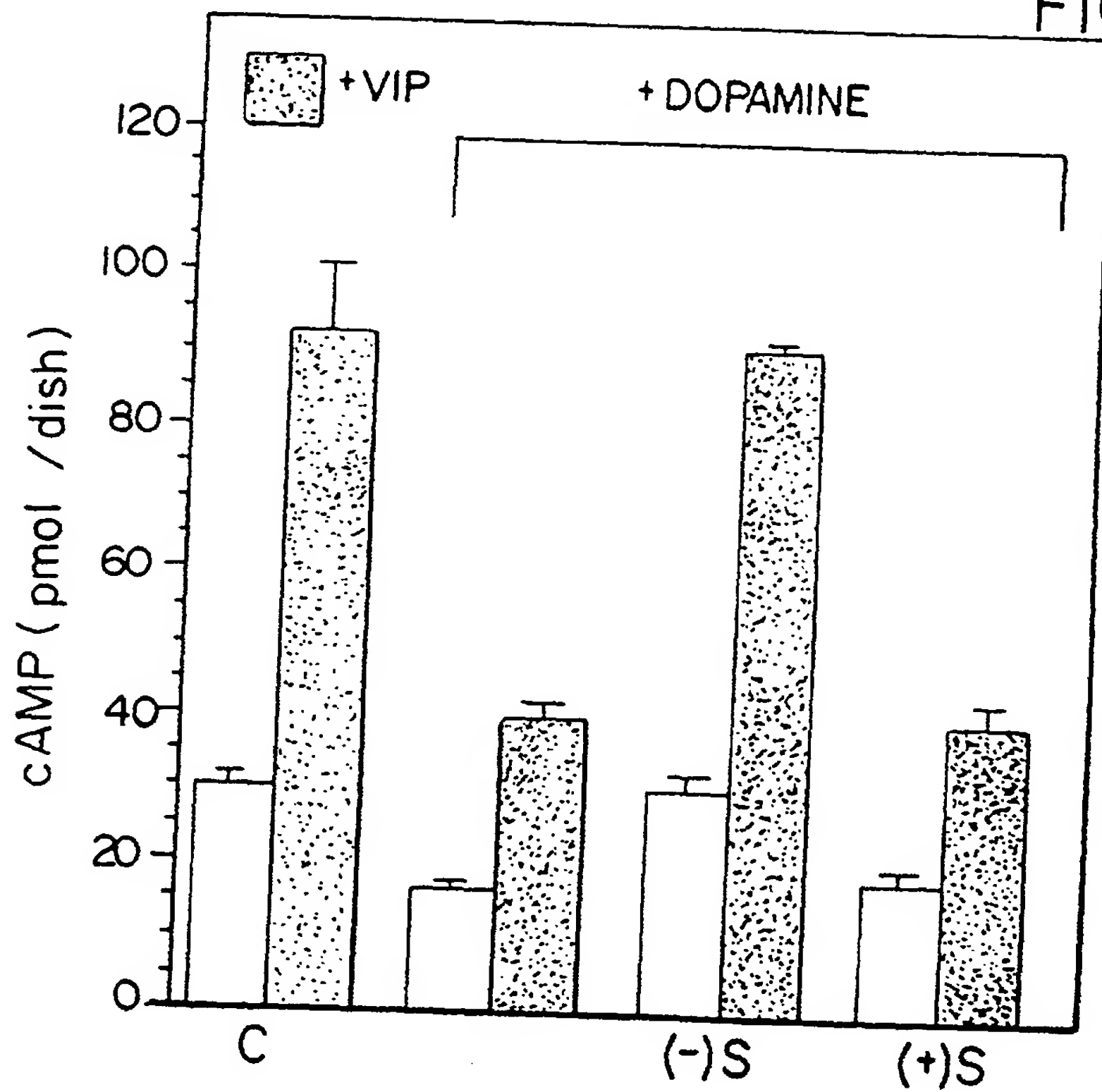
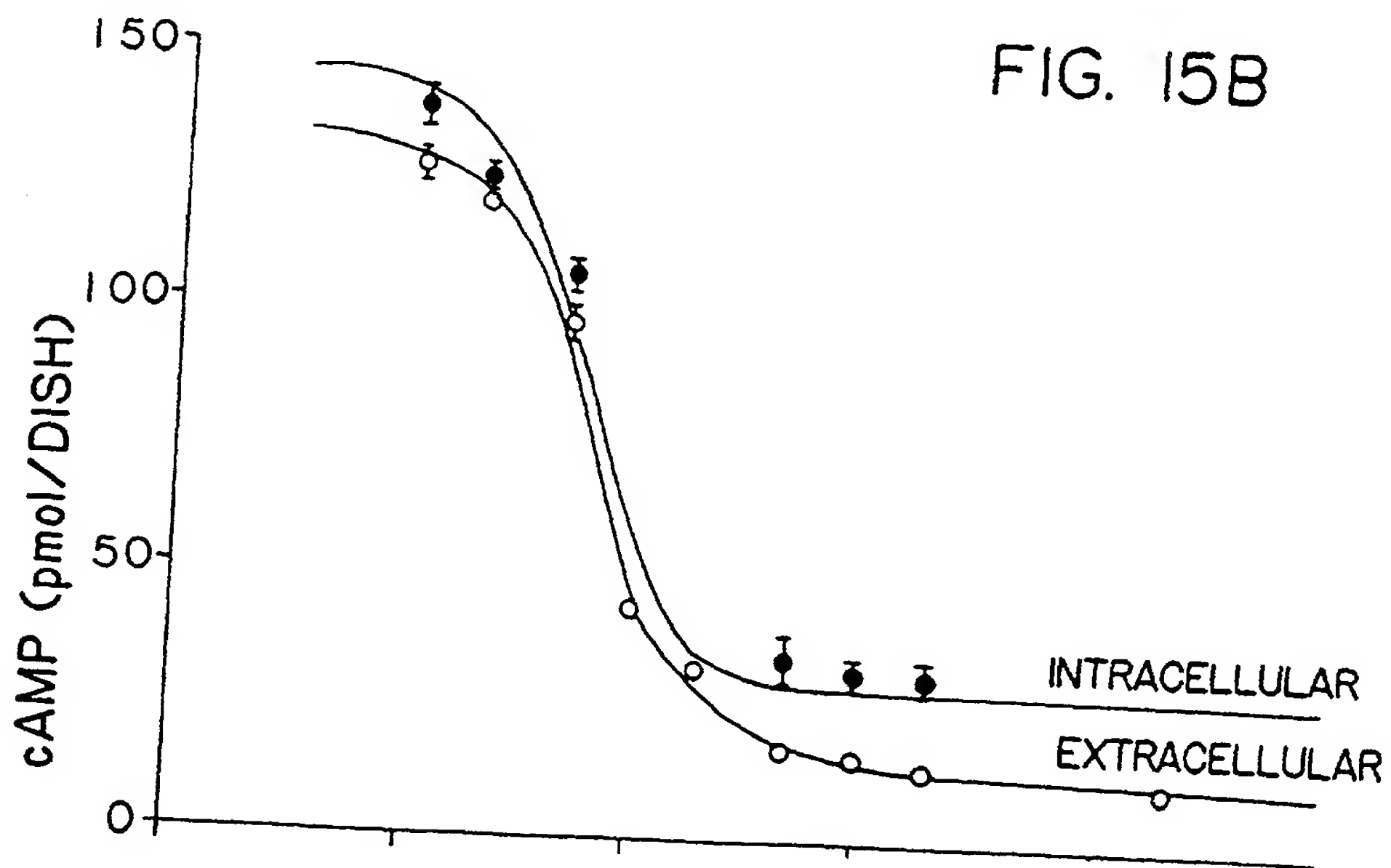
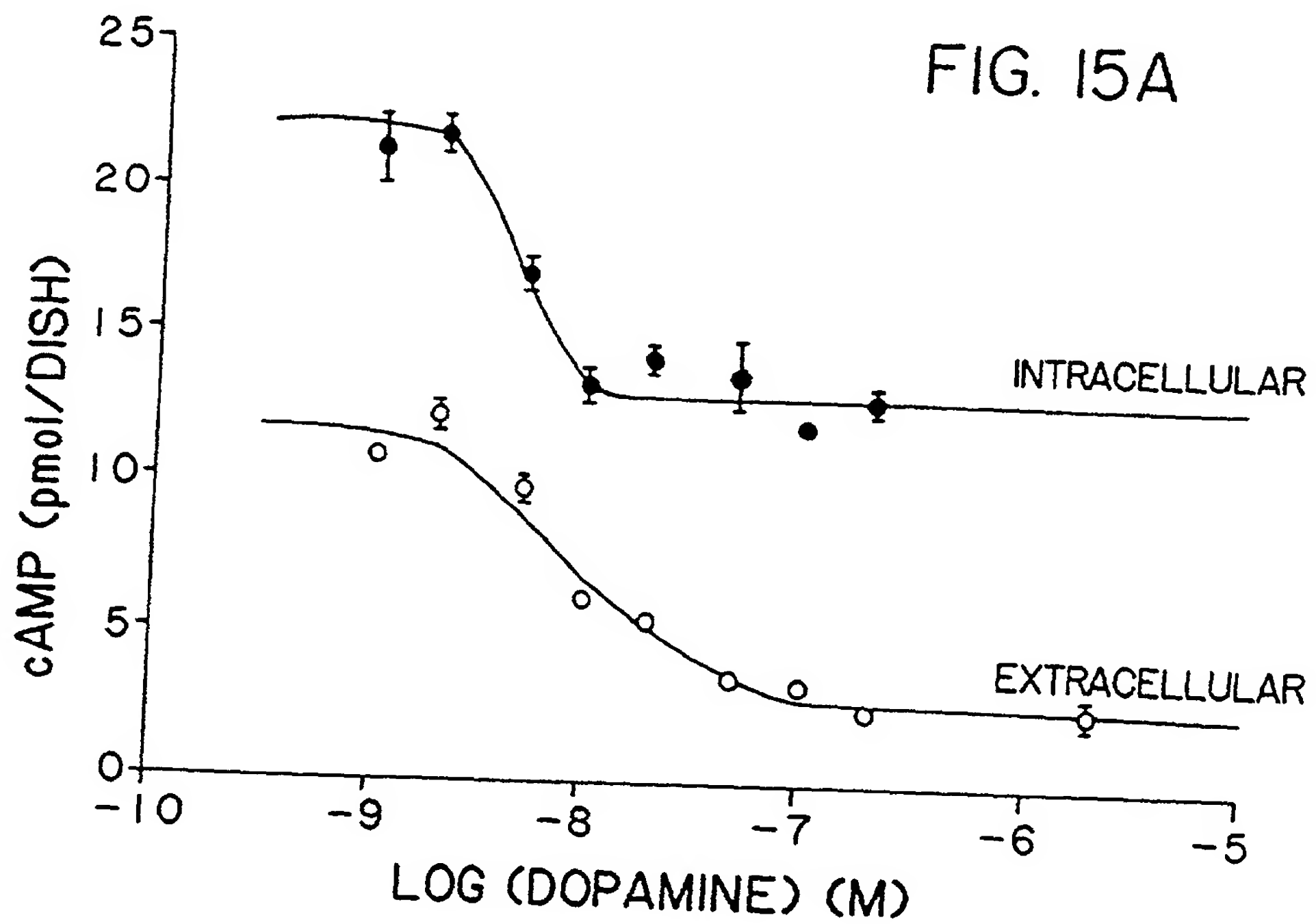


FIG.14B



2025-10-27 14:23:53



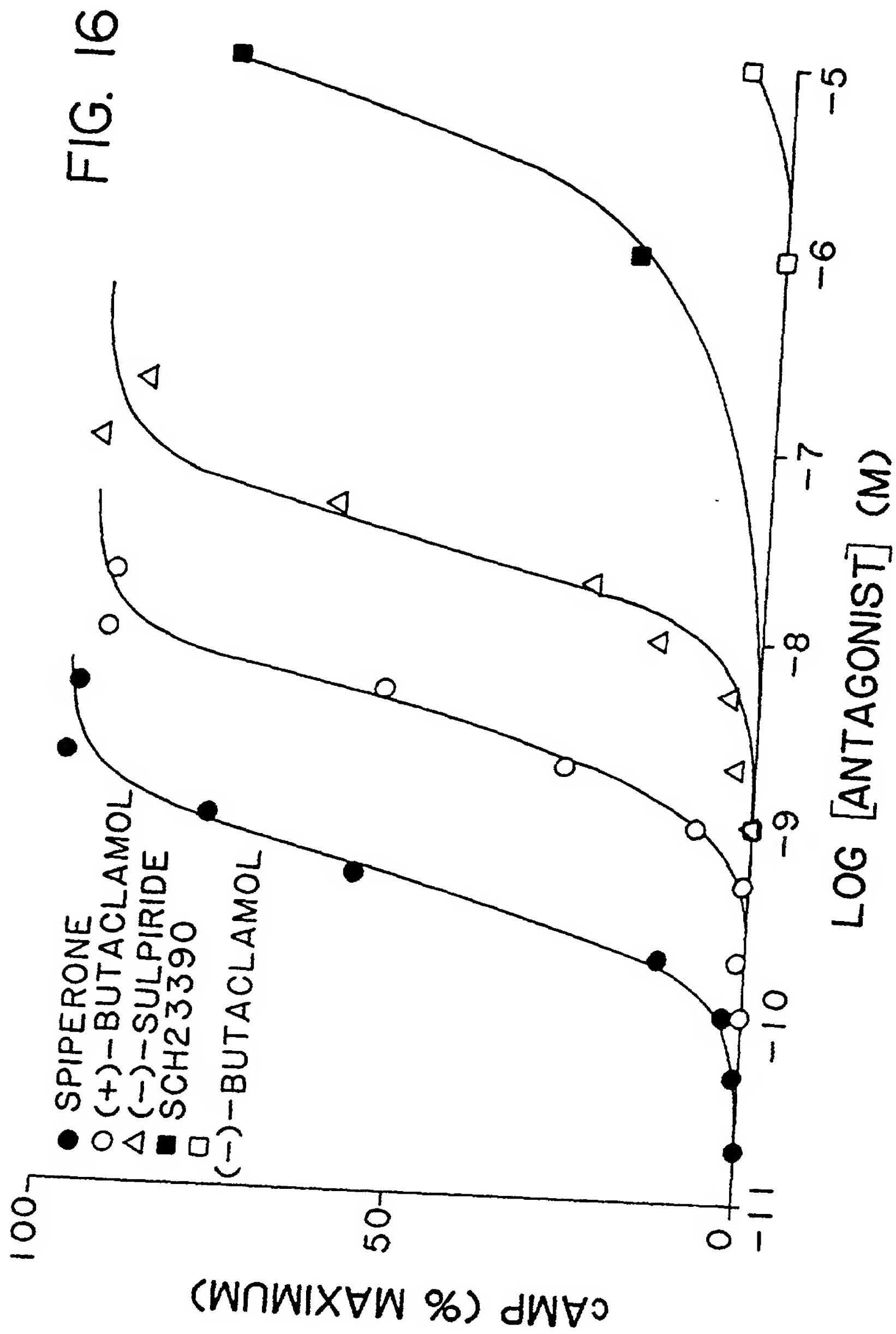


FIG.17A

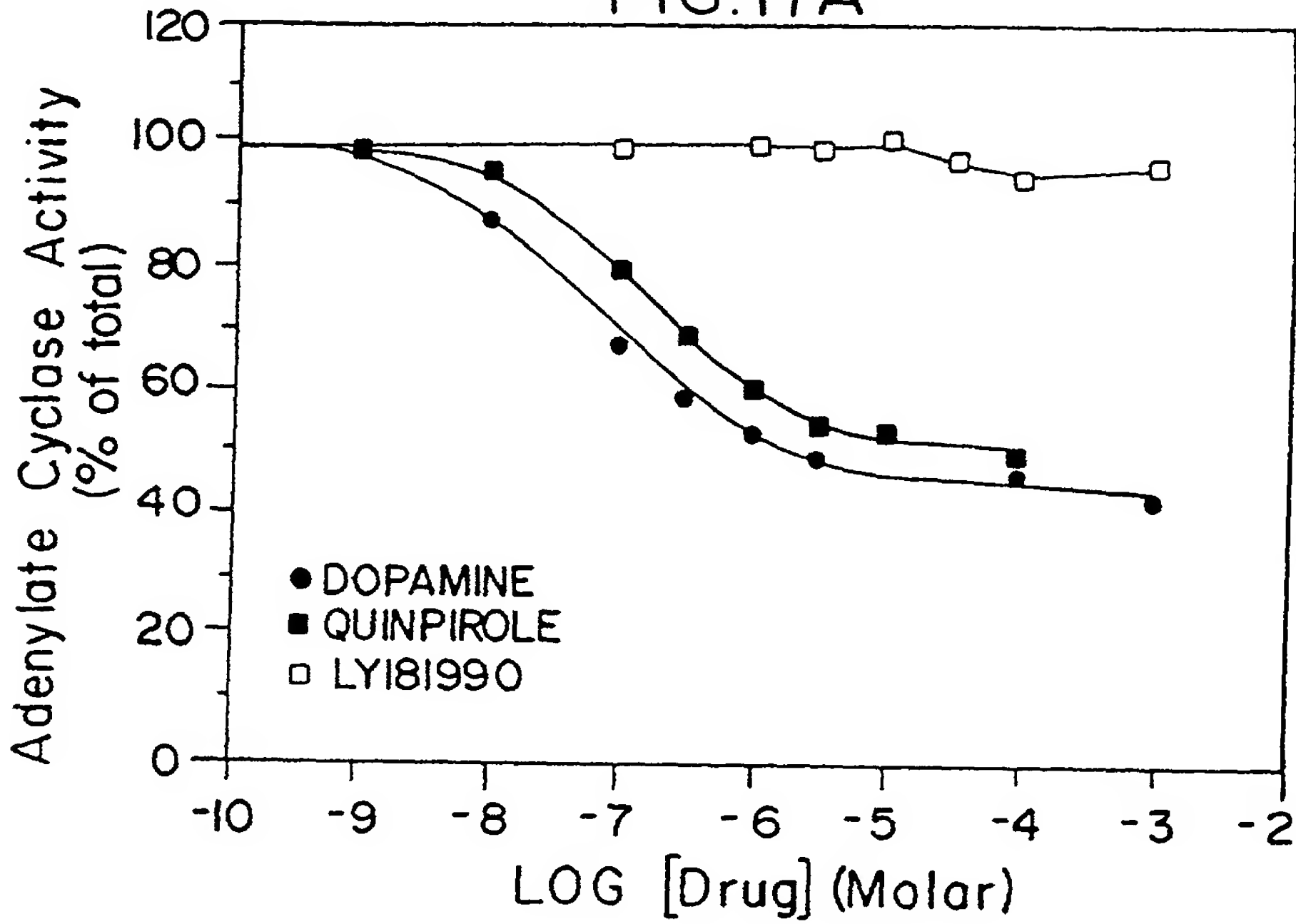
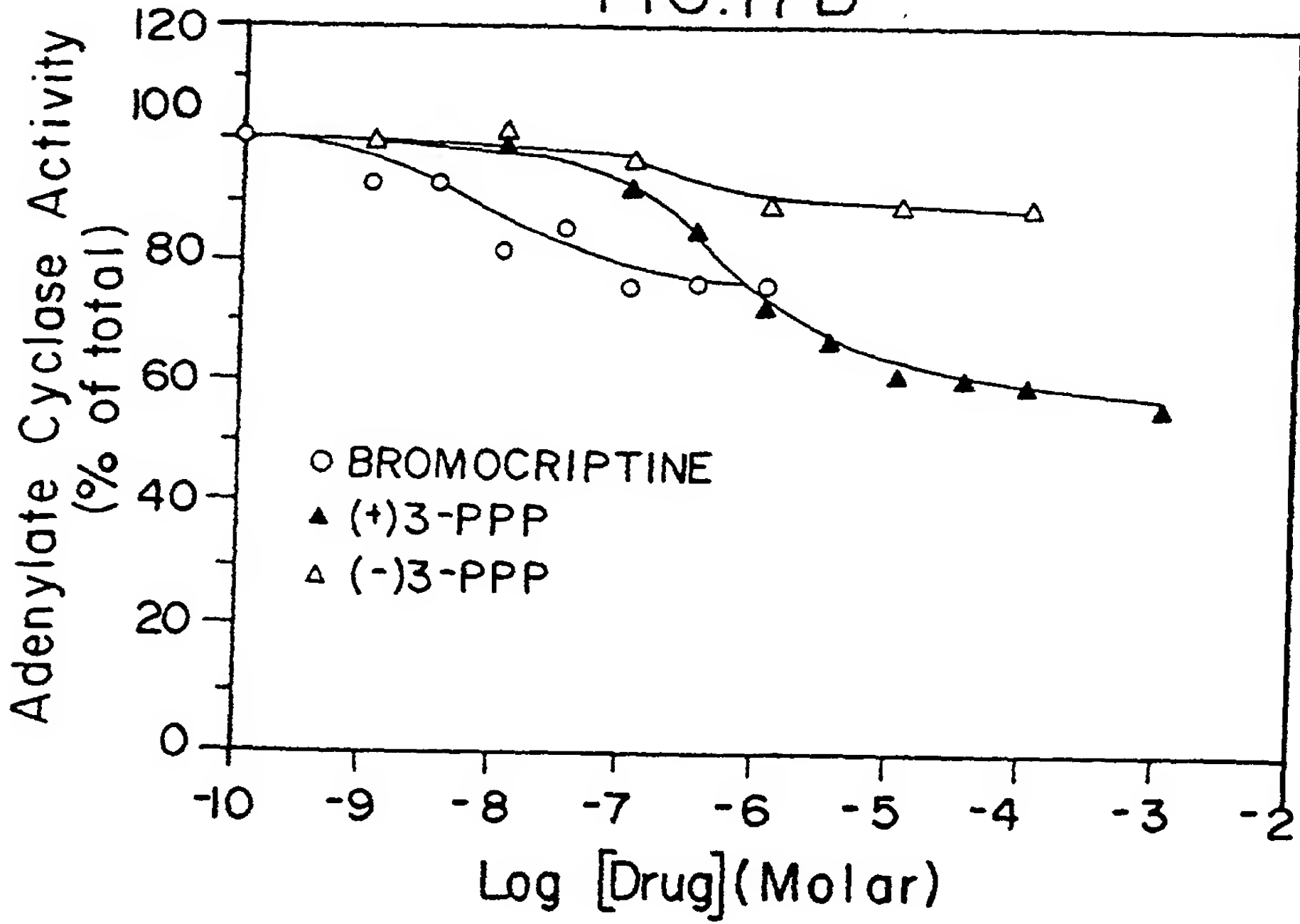


FIG.17B





```

-33 AGAGCCTGGCCACCCAGTGGCTCCACCGCCCTG

*
METAspProLeuAsnLeuSerTrpTyrAspAspLeuGluArgGlnAsnTrpSerArg
10 20
ATGGATCCACTGAATCTGTCCTGGTATGATGATCTGGAGAGGCAGAACTGGAGCCGG
|||||
ATGGATCCACTGAACCTGTCCTGGTACGATGACGATCTGGAGAGGCAGAACTGGAGCCGG
*
ProPheAsnGlySerAspGlyLysAlaAspArgProHisTyrAsnTyrTyrAlaThrLeu
30 40
CCCTTCAACGGGTCAGACGGGAAGCGGACAGACCCCACTACTATGCCACACTG
|||||
CCCTTCAATGGGTCAGAAAGGAAGGCAGACAGGCCCACTACAACACTATGCCATGCTG
120
Glu
MET

```

FIG. 18A

| 50 60  
LeuThrLeuLeuIleAlaValIleValPheGlyAsnValLeuValCysMETAlaValSer  
 CTCACCTGCTCATCGCTGTCATCGTCTTCGGCAACGTGCTGGTGTGCATGGCTGTGTCC  
 IIIIIII IIIII IIIII IIIII IIIII IIIII IIIII IIIII IIIII IIIII  
 CTCACCTCCTCATCTTATCATCGTCTTTGGCAATGTGCTGGTGTGCATGGCTGTATCC  
 PheIle  
 ArgGluLysAlaLeuGlnThrThrThrAsnTyr 70 80  
LeuIleValSerLeuAlaValAlaAsp  
 CGCGAGAAGCGCTGCAGACCACCACTACCTGATCGTCAGCCTCGCAGTGGCCGAC  
 II IIIIIII IIIII IIIII IIIII IIIII IIIII IIIII IIIII IIIII  
 CGAGAGAAGGCTTGCAGACCACCACTACTTGTATAGTCAGCCTTGCTGTGGCTGAT  
 240

90 100  
LeuLeuValAlaThrLeuValMETProTrpValValTyrLeuGluValValGlyGluTrp  
 CTCCTCGTCGCCACACTGGTCAATGCCCTGGGTTGTCTACCTGGAGGTGGTGTAGGTGAGTGG  
 II II IIIII IIIII IIIII IIIII IIIII IIIII IIIII IIIII IIIII  
 CTTCTGGTGGCCACACTGGTAATGCCGTGGGTTGTCTACCTGGAGGTGGTGGTGGTGGTGG

FIG. 18B

[illegible][illegible]

|   |     |     |
|---|-----|-----|
|   | 150 | 160 |
| LeuTyrAsnThrArgTyrSerLysArgArgValThrValMETIleSerIleValTrp     |     |     |
| CTGTACAATACGCGCTACAGCTCCAAGCGCCGGTCACCGTCATGATCTCCATCGTCTGG   | .   | .   |
| IIIII II II IIIIIIIIIIIIIIIII III IIIIIIIII IIIII IIIIIII     |     |     |
| CTGTATAACACACGCTACAGCTCCAAGCGCCGAGTTACTGTCA TGATTGCCATTGTCTGG |     |     |
|   |     | Ala |
|   |     | 480 |

FIG. 18C

## 170

[illegible]

210  
ProPheIleValThrLeuLeuValTyrIle LysIleTyrIleValLeuArgArgArg  
 220  
 CCCTTCATTGTCACCCCTGCTGGTCTACATCAAGATCTACAT<sup>.</sup>GTCTCCTCCGCAGACGCCGC  
 !!!!!!! !!!!!!! !!!!!!! !!!!!!! !!!!!!! !!!!!!!  
 CCCTTCATCGTCACTCTGCTGCTATATCAAAATCTACATCGTCTCCGGAAGCGCCGG  
 Lys

**FIG. 18D**

230 240  
 LysArgValAsnThrLysArgSerArgAlaPheArgAlaHisLeuArgAlaProLeu  
 AAGCGAGTCAACACCAACGACGAGCCGAGCTTTCAGGGCCACCTGAGGGCTCCACTA  
 !!!!! !!!!! !!!!! !!!!! !!!!! !!!!! !!!!! !!!!! !!!!!  
 AAGCGGTCACACCAACGCGCAGTCGAGCTTTCAGAGCCAACTGAAGACACCACTC  
 Asn LysThr 720

\* 250 \*  
 LysGlyAsnCysThrHisProGluAspMETLysLeuCysThrValIleMETLysSerAsn  
 ▼ AAGGGCAACTGTACTCACCCGAGGACATGAAACTCTGCACCGTTATCATGAAGTCTAAT  
 !!!  
 AAG.....

270 280  
 GlySerPheProValAsnArgArgArgValGluAlaAlaArgArgAlaGlnGluLeuGlu  
 GCGAGTTTCCAGTGAACAGCGGAGAGTGGAGGCTGCCCGCGAGCCAGGAGCTGGAG  
 !! !!!!! !!!!! !!!!! !!!!! !!!!! !!!!! !!!!!  
 .....GATGCTGCCCGCGAGCTCAGGAGCTGGAA 840  
 Asp

FIG. 18E

|  |               |
|--|---------------|
| 290  | 300           |
| METGluMETLeuSerSerThrSerProProGluArgThrArgTyrSerProIleProPro |               |
| ATGGAGATGCTCTCCAGCACCCAGCCCGAGAGACCCGGTACAGCCCATCCACCC       |               |
| IIIIIIIIII II IIIIIIIIIII II IIIIIIIIIII IIIIIIIIIII III     |               |
| ATGGAGATGCTGTCAAGCACCCAGCCCGAGAGAGACCCGGTATAGCCCATCCCTCCC    |               |
| 310  | 320           |
| SerHisHisGlnLeuThrLeuProAspProSerHisHisGlyLeuHisSerThrProAsp |               |
| AGCCACCACGCTGACTCTCCCGACCCGTCCTCCACCATGGTCTCCACAGCACTCCCGAC  |               |
| II IIIIIIIIIII IIIIIIIIIII IIIIIIIIIII III IIIIIII III       | 960           |
| AGTCACCACGCTCACTCTCCCTGATCCATCCACCGCCTACATAGCAACCCCTGAC      |               |
|  | Asn           |
| 330  | 339           |
| SerProAlaLysProGluLysAsnGlyHisAlaLys AspHisProLysIleAlaLys   |               |
| AGCCCCGCCAAACAGAGAAATGGGCATGCCAAA...GACCAACCAAGATTGCCAAG     |               |
| II II IIIIIIIIIII IIIIIIIIIII IIIIIII IIIIIIIIIII III        |               |
| AGTCCTGCCAAACAGAGAAATGGGCACGCCAAGATTGTCAATCCAGGATTGCCAAG     |               |
|  | IleValAsn Arg |

FIG. 18F

[illegible][illegible][illegible]

**FIG. 18G**



Vll 419

|                    |  |     |     |
|--------------------|--|-----|-----|
| AspCysAsnIleProPro | ValLeuTyrSerAlaPheThrTrpLeuGlyTyrValAsnSer | VII | 419 |
|--------------------|--|-----|-----|

.  
GACTGCAACATCCCGCCTGTCCCTGTACAGCGGCCTTACAGTGGCTATGTCAACAGC  
|| ||||||| || ||||| ||||||| ||||||| ||||||| |||||||  
GATTGCAACATCCCACCAGTCCTCTACAGCGCCTTCACATGGCTATGTCAACAGT

439

AlaValAsnProIleIleTyrThrThrPheAsnIleGluPheArgLysAlaPheLeuLys

IleLeuHisCys \*  
GCCGTAACCCCATCTACACCACCTTCAACAATTGAGTTCCGCAAGGCCTTCCTGAAG  
IIIIII IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII IIIIII  
GCCGTCAAACCCCATCTACACCACCTTCAACATCGAGTTCCGCAAGGCCTTCATGAAG  
MET

1317

ATCCTCCACTGCTGACTCTGCTGCTGCCCGCACAGCAGCCTGCTTCCACCTCCCTGCC  
 ||| | ||| ||| ||| |||  
 ATCTTGCACTGCTGA

FIG. 18H



CAGGCCGGCCAGCCTCACCCCTTGCGAACCGTGAGCAGGAAGCCTGGGTGGATCGGCCTC 1437

CTCTTCTTAGCCCCGGCAGGCCCTGCAGTGTTGCTTGGCTCCATGCTCCTCACTGCCCG

CACACCTCACTCTGCCAGGGCAGTGCTAGTGAGCTGGGCATGGTACCAGCCCTGGGGCT 1557

GGCCCCAGCTCAGGGGCAGCTCATAGAGTCCCCCTCCACCTCCAGTCCCCCTATCCTT

GGACCAAGATGCAGCCGCCCTTCCTTGACCTTCCTCTGGGGCTCTAGGGTTGCTGGAGC 1677

CTGAGTCAGGGCCAGAGGCTGAGTTTTCTCTTTGTGGGGCTTGGCGTGAGCAGCGGT

GGGGAGAGATGGACAGTTCACACCCCTGCAAGGCCACAGGAGGCAAGCAAGCTCTTGC 1797

CGAGGAGCCAGGCAACTTCAGTCCTGGGAGACCCATGTAAATACCAGACTGCAGTTGGA

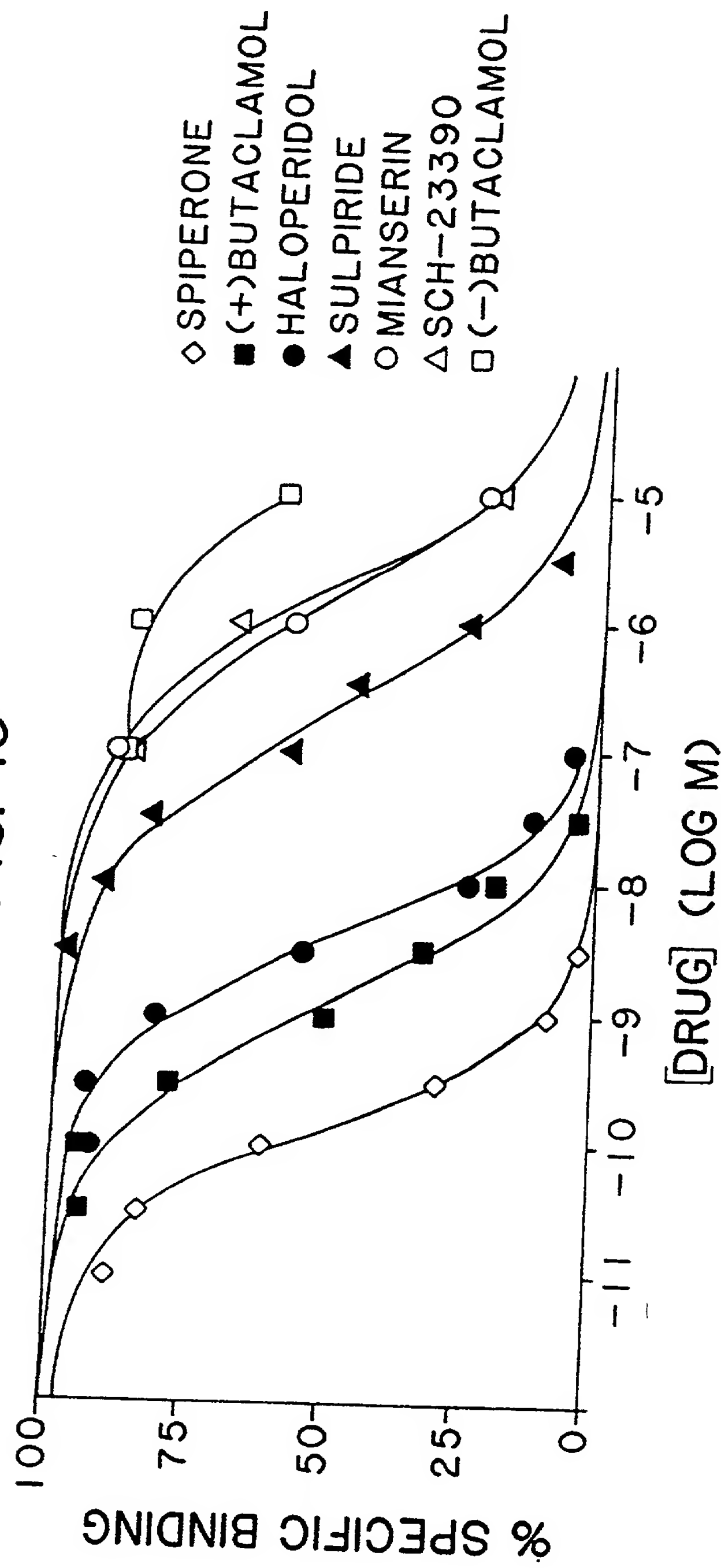
CCCCAAGGATTCCCAAGCCAAACCTTAGCTCCCTCCCGCACCCCGATGTGGACCTCTA 1917

FIG. 18I

CTTCCAGGCTAGTCCGGACCCACCTCACCCTTACAGCTCCCAAGTGGTTTCCACAT  
GCTCTGAGAAGAGGCCCTCATCTTGAAGGGCCAGGAGGTCTATGGGAGAGGAACT 2037  
CCTTGGCCTAGCCACCCCTGCTGCCCTTCTGACGGCCCTGCAATGTATCCCTTCTCACAGC  
ACATGCTGGCCAGCCCTGGGGCCTGGCAGGAGGTCAGGCCCTGGAACTCTATCTGGGCCT 2157  
GGCTAGGGACATCAGAGGTTCTTTGAGGGACTGCCCTCTGCCACACTCTGACGCAAAACC  
ACTTCCCTTTCTATTCTCTGCCCTTCCCTCTCTCCTGTTTCCCTTCCCTTCCACTGC 2277  
CTCTGCCCTTAGAGGAGCCACGGCTAAGAGGCTGCTGAAAACCATCTGGCCTGGCCTGGC  
CCTGCCCTGAGGAAGGAGGCAAGCTGCAGCTTGGGAGAGCCCCTGGGCCTAGACTCTG 2397  
TAACATCACTATCCGATGCACCAACTAATAAACTTTGACGAGTCACCTTC (A)<sub>n</sub> 2449

FIG. 18J

FIG. 19



1 2 3 4

kb

—12.0

— 6.0

— 4.0

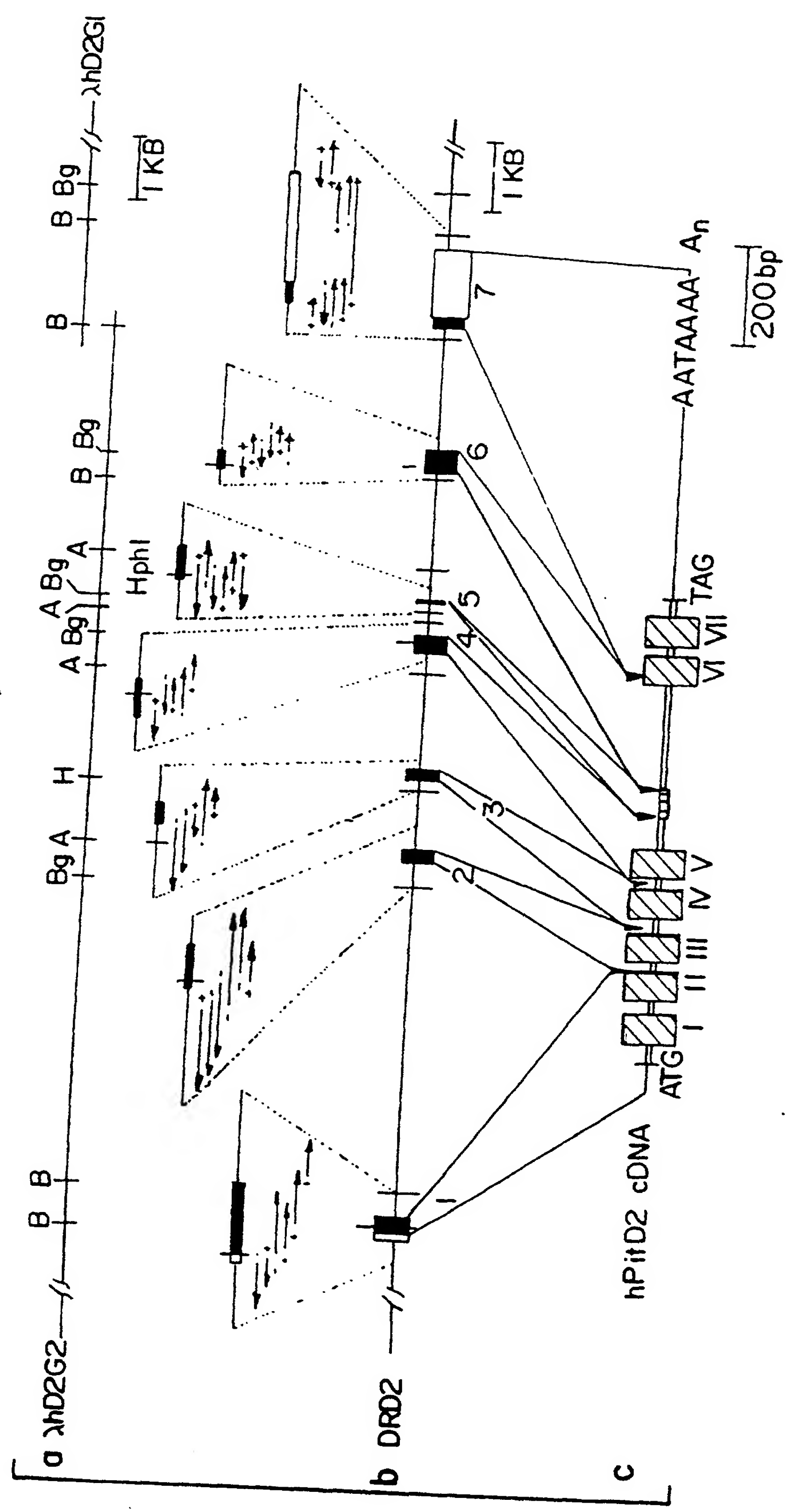
— 2.0

— 1.6

— 1.0

FIG. 20

FIG. 21



2025-03-20 15:23:00

| DRUG   | HUMAN D <sub>2</sub> | RAT D <sub>2</sub> | RAT STRIATUM |
|--|----------------------|--------------------|--------------|
| PIPERONE                                     | 0.125                | 0.35               | 0.56         |
| (+) BUTACLAMOL                               | 0.94                 | 1.2                | 1.6          |
| HALOPERIDOL                                  | 2.4                  | 5.1                | 5.8          |
| SULPIRIDE                                    | 206                  | 160                | 205          |
| MIANSERIN (5-HT)                             | 2685                 | 4300               | 4600         |
| SCH 23390 (DI)                               | 2145                 | 2500               | 3300         |
| (+) BUTACLAMOL                               | >10,000              | >10,000            | >10,000      |
| K <sub>d</sub> [ <sup>3</sup> H] DOMPERIDONE | 0.74                 | 0.40               | 0.40         |

FIG. 22

FIG. 23

|                        |                                |
|------------------------|--------------------------------|
| 2851                   | 286                            |
| exon1...GCAGgtagtg...  | introns...tccccagGTGG...exon2  |
| 395                    | 396                            |
| exon2...ACAGgtgagcc... | introns...cttgcagGTAC...exon3  |
| 532                    | 533                            |
| exon3...GCAGgtacatt... | introns...ccccccagACCA...exon4 |
| 723                    | 724                            |
| exon4...AAAGgtctcaa... | introns...tccacagGGCA...exon5  |
| 810                    | 811                            |
| exon5...AGTGgtaagt...  | introns...ggcgcagGAGG...exon6  |
| 1138                   | 1139                           |
| exon6...CTCGgtgagtc... | introns...ccccccagGCGT...exon7 |

<sup>1</sup>Numbering begins with A of the putative initiator methionine codon (see Fig. 18)